#### STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To:

Wednesday, January 16, 2002 1:54 PM Li, Janice; STIC-Biotech/ChemLib

Subject:

RE: rush search for 09/242,202

### Please rush. Thanks Chris

----Original Message-----Fr m:

Li, Janice

Sent:

Wednesday, January 16, 2002 1:26 PM

T :

Chan, Christina

Subject:

rush search for 09/242,202

Hi, Chris:

Could you please give approval for rush search SEQ ID Nos: 10, 16, 22, 27, 28; residues 1-12 of SEQ ID No: 22; and residues 1-11 of SEQ ID No: 10 against all commerical databases including pending patent database.

This is an amended case.

Thanks,

Q. Janice Li Patent Examiner AU 1632 CM1, Rm12D11 Mail Box12E12 703-308-7942 janice.li@uspto.gov

Point of Contact: Mona Smith Technical Info. Specialist CM1 12C14 Tel: 308-3278

Searcher: M. Sai, 74
Phone:
Location:
Date Picked Up: 1/17/02
Date Completed: 1118
Searcher Prep/Review:/ S
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences: 7
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.) STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Tochard Countries

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TITLE OF INVENTION: SYSTEM FOR GENERATING RECOMBINANT VIRUSES FILE REFERENCE: PU3481US2 CURRENT APPLICATION NUMBER: US/09/309,382 CURRENT FILING DATE: 1999-05-10 EARLIER APPLICATION NUMBER: 60/084,936 EARLIER FILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 26
                                                                     ; Search time 221.34 Seconds
(without alignments)
12.279 Million cell updates/sec
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Sequence 8, Appli
Sequence 24, Appl
Sequence 25, Appl
Sequence 8, Appli
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Sequence 13, A
Sequence 17, A
Sequence 18, A
Sequence 9, Ap
Sequence 9, Ap
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Sequence 17, P
Sequence 8, Ap
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PGTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-987-418A-9
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US-09-309-382-17
US-09-309-382-18
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US-08-388-653-4
US-08-473-985-4
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                                                                                                                    US-09-242-202A-22_COPY_1_12
1 GCCACCATGGCC :12
                                                                      January 17, 2002, 11:54:39
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
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8-4 Sequence 4, Appli 3-4 Sequence 4, Appli 3-4 Sequence 4, Appli 0-4 Sequence 4, Appli 1-4 Sequence 4, Appli 0-4 Sequence 4, Appli 0-4 Sequence 4, Appli 0-4 Sequence 6, Appli 3B-6 Sequence 6, Appli 3B-6 Sequence 6, Appli 3B-6 Sequence 6, Appli 3B-1 Sequence 7, Appli 3B-1 Sequence 7, Appli 3B-1 Sequence 7, Appli 3B-1 Sequence 20, Appli 3B-1 Sequence 21, Appli 3B-1 Sequence 22, Appli 3B-1 Sequence 22, Appli 3B-1 Sequence 23, Appli 3B-1 Sequence 32, Appli 3B-1 Sequence 32, Appli 3B-1 Sequence 32, Appli 3B-1 Sequence 33, Appli 3B-1 Sequence 34, Appli 3B-1 Sequence 35, Appli 3B-1	unknown or other Sequence: synthetic	Length 15; 2; 0; Indels 0; Gaps 0;	NT VIRUSES
20	unkr Sequé	2,:	
S-08-483-89 SS-09-087-71 SS-09-157-23 SS-09-157-23 SS-09-158-01 SS-09-158-01 SS-09-158-01 SS-09-158-01 SS-09-38-01 SS-09-309-38 SS-09-309-38 SS-09-309-38 SS-09-309-38 SS-09-309-38 SS-09-309-38 SS-09-309-38 SS-08-425-68 SS-08-4	be A, T, C, G, of Artificial tide	Score 12; DB 4; Pred. No. 6.7e+0 0; Mismatches	on US/09309382 Cynthia Cynthia Sysbren FOR GENERATING RECOMBINANT VIRUSES
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28 12 29 12 33 30 12 33 12 33 12 12 33 34 12 34	IN. LONA ISM: A. ISM: A. INFOR INFOR INFOR INFOR INFOR	Match Local Sines 12; 16 GCCAC	2 -382-8 e 8, A NO. 62 INFOR ANT: R ANT: W
28 12 100. 29 12 100. 31 12 100. 31 12 100. 32 12 100. 33 12 100. 34 12 100. 35 12 100. 36 12 100. 37 12 100. 38 12 100. 39 12 100. 40 12 100. 41 12 100. 44 12 100. 45 12 100. 46 12 12 100. 47 12 100. 48 12 100. 48 12 100.	TYPE: DNA CRGANISM: FEATURE: FEATURE: COTHER INF: COTHER INF: COTHER INF: COTHER INF: COTHER INF: COTHER INF:	Query Match Best Local ( Matches 1:) Qy 1 GCG Db 4 gcG	RESULT 2 US-09-309-382-8 ; Sequence 8, A ; Patent No. 62 ; GENERAL INFOR ; APPLICANT: W ; TITLE OF INV

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TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: nucleic acid
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COUNTRY: USA
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US-08-013-801-8
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TELEX: 2
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                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: recognition US-09-309-382-8
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US-09-309-3182-25/c
| Sequence 25, Application US/09309382
| Sequence 25, Application US/09309382
| Patent No. 6291214
| GENERAL INFORMATION:
| APPLICANT: Weiner, Michael
| TILLE OF INVENTION: SYSTEM FOR GENERATING RECOMBINANT VIRUSES
| FILE REPERENCE: D93481825
| CURRENT FILING DATE: 1999-05-10
| EARLIER FILING DATE: 1999-05-11
| NUMBER OF SEQ ID NOS: 26
| SOFTWARES PATENTION OF 2.0
| SEQ ID NO 25
| LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Richards, Cynthia APPLICANT: Richards, Michael TITLE OF INVENTION: SYSTEM FOR GENERATING RECOMBINANT VIRUSES FILE REFERENCE: P034081052 CURRENT APPLICATION NUMBER: US/09/309,382 CURRENT FILING DATE: 1999-05-10 EARLIER APPLICATION NUMBER: 60/084,936 EARLIER PILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 26 SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                       Length 18;
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Patent No. 6291214
GENERAL INFORMATION:
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                                                   TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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LENGTH: 22
               SEQ ID NO 8
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CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
FEATURE:
CHER INFORMATION: n bases may be A, T, C, G, unknown or other
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: synthetic
CHER INFORMATION: oligonucleotide
US-09-309-382-25
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                                                                                                                                                                                    Length 22;
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hes 0; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                       DB 4;
                                                                                                                                                                                100.0%; Score 12; DB
100.0%; Pred. No. 6.6
tive 0; Mismatches
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02 FEB 1993
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NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08013801
Patent No. 5420019
GENERAL INFORMATION:
APPLICANT: Theofan, Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
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Horwitz, Arnold
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Baltaian, Manik
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312/346-9740
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APPLICATION NUMBER: US
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Best Local Similarity 100.

Matches 12; Conservative
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INFORMATION FOR SEQ ID NO:
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RESULT
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Patent No. 5447913
Patent No. 5447913
APPLICANT: Little, Roger G. APPLICANT: Ammons, William Steve
APPLICANT: Ammons, William Steve
TITLE OF INVENTION: Increasing Protein Dimer Products
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                                                                                                                                                                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker
                                                                                                                                                                      APPLICANT: Theoran, Georgia
APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
NUMBER OF SQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: 11110.153

ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,063
FILING DATE: 19930519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 1; 100.0%; Pred. No. 6.5e+02;
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: United States of America
                                                                                                                 Sequence 17, Application US/08072063 Patent No. 5439807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Meyers Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 3065!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
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Best Local Similarity 100.
Matches 12; Conservative
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CORRESPONDENCE ADDRESS:
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10 GCCACCATGGCC 21
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                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illlinois
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                                                                                                                                                          GENERAL INFORMATION:
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                                                                             RESULT 6
US-08-072-063-17
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US-08-212-132-8
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APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,693
FILING DATE: 19930519
CLASSIFICATION: 424
NAME: MGYENT INFORMATION:
REGISTRATION NUMBER: 36,989
                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12; DB 1;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 South Wacker CITY: Chicago STATE: Illlinois
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     APPLICATION ...
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 2712;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/4/4-6300
TELEFAX: 312/4/4-6300
TELEFAX: 312/4/4-6300
TELEFAX: 312/4/4-6300
TELEFAX: 32-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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100.0%;
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INFORMATION FOR SEQ ID NO: 17:
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-212-132-8
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GENERAL INFORMATION:
APPLICANT: Little, Roger
APPLICANT: Little, Roger
APPLICANT: Ammons, Steve
TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Dimer Products
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27129/31735
                                                                                                                                                                                                                                                                                                                    CITY: Chicayo
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                Sequence 8, Application US/08470366 Patent No. 5703038
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; Patent No. 5827816
; GENERAL INFORMATION:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
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                                                                           US-08-470-366-8
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APPLICANT: Theoran, Georgia
APPLICANT: Horvitz, Arnold
APPLICANT: Burke, David
APPLICANT: Burke, David
APPLICANT: Grinna, Lynn S.
TITLE OF INVENTION: Stable Bactericidal/Permeability-Increasing
TITLE OF INVENTION: the Same
TITLE OF INVENTION: the Same
TITLE OF EQUENCES: 14
CORRESPONDENCES ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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6300 Sears Tower, 233 South Wacker Drive
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,417
                                                                                                                                                                                         100.0%; Score 12; DB 1; 1 100.0%; Pred. No. 6.5e+02;
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NAME: Meyers, Thomas C.
REGISTRATION NUMBER: p-36,989
REFERENCE/DOCKET NUMBER: 27129/30911
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08430417
Patent No. 5674834
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                 TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-064-693-17
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Best Local Similarity
Matches 12; Conserv
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STRANDEDNESS:
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US-08-430-417-8
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APPLICANT: Burke, David

APPLICANT: Burke, David

APPLICANT: Baltaian, Manik

APPLICANT: Grinna, Lynn S.

TITLE OF INVENTION: Stable Bactericidal/Permeability-Increasing

TITLE OF INVENTION: Protein Products and Pharmaceutical Compositions Containing

TITLE OF INVENTION: The Same

NUMBER OF SEQUENCES: 14
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                                                                    Gaps
100.0%; Score 12; DB 1; Length 27; 100.0%; Pred. No. 6.5e+02; ive 0; Mismatches 0; Indels
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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312/474-0448
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60606-6402
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US-08-704-504-8
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    TELEPHONE:
                                                                                                                                                            TOPOLOGY:
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US-08-885-366-17
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Sequence 8, Application US/08704504
Patent No. 5856302
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Ammons, William Steve
TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Dimer Products
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5e+02;
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100.0%; Pred. No. (
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NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 27129/31735
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              27129/30911
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APPLICATION NUMBER: US/08/212,132
FILING DATE:
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COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REFERRACION NUMBER: 27129/3
REFERRACE/DOCKET NUMBER: 27129/3
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEQ
                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                            COMPUTER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 12; Conserv
Illinois
                                    60606-6402
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CLASSIFICATION:
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CITY: Chicago
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US-08-466-822-8
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                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Theofan, Georgia
APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 4; L
100.0%; Pred. No. 6.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                          100.0%; Score 12; DB 2; 100.0%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker CITY: Chicago
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08885366 Patent No. 6274348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                 LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 12; Conservative
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ADDRESSEE:
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                                                                                                          Sequence 8, Application US/09223342
Patent No. 6277821
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Ammons, William Steve
TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Dimer Products
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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6300 Sears Tower, 233 South Wacker Drive
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100.0%; Score 12; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 17, Application PC/TUS9304754
SERVERAL INFORMATION:
APPLICANT: Theofan, Georgia
APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INFORTION:
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   Marshall, O'Toole, Gerstein, Murray &
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,504
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFRENCE/COCKT NUMBER: 2712;
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: 312/4/4-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
1 GCCACCATGGCC 12
                 10 GCCACCATGGCC 21
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; MOLECULE TYPE: CDNA
US-09-223-342-8
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US-09-223-342-8
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Pred. No. 6.5e+02;
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19930519
CLASSIEICATION:
ATTORNEY/AGENT INPORMATION:
NAME: MAYORS C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 36,980
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAR: 312/474-6300
TELEFAR: 312/474-6300
TELEFAR: 312/474-6300
1: Borun
6300 Sears Tower, 233 South Wacker
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
               STREET: 6300 Sears
CITY: Chicago
STARE: 1111inois
COUNTRY: USA
ZIP: 60606-6402
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STRANDEDNESS: sinq]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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PCT-US93-04754-17
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AX139440 Sequence AX098902 Sequence AX099322 Sequence AR027668 Sequence AR050743 Sequence AX030652 Sequence

AX099322 AR027668 AR050743 AX030652

AX139440 AX098902

Description

OM nucleic

Run on:

Sednence:

Title:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human g protein-coupled receptor, pfi-010
Patent: EP 1094109-A 3 25-APR-2001;
Pfizer Limited (GB): PFTZER INC. (US)
Location/Qualifiers
//organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX139440 22 bp DNA
Sequence 3 from Patent EP1094109.
AX139440 GI:14275086
        DB
         Length
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Query
Match 1
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                                  human.
         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AX139440
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                          ; Search time 10436.3 Seconds
(without alignments)
18.969 Million cell updates/sec
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                                                                                                                                                                               2944280
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                            1472140 segs, 8248589755 residues
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                                                           January 17, 2002, 11:49:53
                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htgo_rod:*
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Maximum DB seq length: 200000000
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gb_n:*
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AR053605 AR053608 AR131268

AR040950 AR051818

AX114583 AX088738

AX077144 AX099890

AX138011

AX049981

184665

113573 Sequence 17
168187 Sequence 18
162302 Sequence 18
AX17923 Sequence 18
AX17923 Sequence 18
AX17923 Sequence 18
AX17929 Sequence 18
AX051809 Sequence 18
AX051809 Sequence 18
AX051809 Sequence 6
AX13318 Sequence 6
AX1734 Sequence 6
AX09819 Sequence 6
AX09813 Sequence AX088738 Sequence AX088738 Sequence AX088738 Sequence AX088738 Sequence AX114583 Sequence AX085608 Sequence AX0851818 Sequence AX0851818 Sequence AX051818 Sequence AX115993 Sequen

AR035389 AR050804 AR053809

AR146549

AR091590 AR117469 AR141722 AX103386 I35208 Sequence 10 A97024 Sequence 1 AXI33393 Sequence ARO40909 Sequence

30-MAY-2001

PAT

source

SUMMARIES

FEATURES

ALIGNMENTS

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1 (bases 1 to 27)
Ammons, W.Steve and Little, R.G.
Ammons, W.Steve and Little, R.G.
Therapeutic uses of bactericidal/permeability-increasing protein
dimer products
Patent: US 5856302-A 8 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 27)
Theofan,G., Horwitz,A., Burke,D., Baltaian,M. and Grinna,L.
Stable bactericidal/permeability-increasing protein products and
pharmaceutical compositions containing the same
Patent: US 5827816-A 8 27-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
   100.0%; Score 12; DB 6; Length 23; 100.0%; Pred. No. 2.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 12; DB 6; Length 27; 1 Similarity 100.0%; Pred. No. 2.3e+04; 12; Conservative 0; Mismatches 0; Indels
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                                  0; Mismatches
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                                                                                                                                                                      AR027668 27 bp DNA
Sequence 8 from patent US 5856302.
AR027668 GI:5938488
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Sequence 8 from patent US 5827816.
AR050743
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10 c 9 q
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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                                 12; Conservative
                                                                                3 GCCACCATGGCC 14
                                                               1 GCCACCATGGCC 12
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Unclassified.
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Matches 12; Conserv
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   Query Match
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VERSION
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VERSION
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AR027668
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AR050743
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AX030652
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                                                                                                                                                                                                                                                                                                                                  artificial sequence.

1 (bases 1 to 23)

Brown, J.P. and Bertelli, F.

Secreted soluble _g(a)2_g(a)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4

calcium channel subunit polypeptides and screening assays using
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 23)
Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
                                                                                                                                                                                                                                  02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-2001
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Screening for alpha2delta-1 subunit binding ligands
Patent: WO 0120335-A 27 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
LOCATION/QUALIFIERS
                                                               Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
                                                                                            Indels
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                                                            100.0%; Score 12; DB 6; I
100.0%; Pred. No. 2.4e+04;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.4e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
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/db_xref="taxon:32630"
/note="primer"
                                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 0119870-A 27 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
Location/Qualifiers
                                                                                                                                                                                                                              AX098902 23 bp DNA
Sequence 27 from Patent W00119870.
AX098902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX099322 23 bp DNA
Sequence 27 from Patent WO0120336.
AX099322
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1 (bases 1 to 27)
Theofan,G., Horwitz,A., Burke,D., Baltalan,M. and Grinna,L. Stable bactericidal/permeability-increasing protein products and pharmaceutical compositions containing the same Patent: US 5674834-A 8 07-007-1997;
Location/Qualifiers
Therapeutic uses of bactericidal/permeability-increasing protein
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Theofan,G., Grinna,L.S. and Horwitz,A.
BPI-immunoglobulin fusion proteins
Patent: US 5643570-A 17 01-JUL-1997;
Location/Qualifiers
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             dimer products
Patent: US 5447913-A 8 05-SEP-1995;
Location/Qualiflers
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150683
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                                                                     /organism="unknown"
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                                                                                                             1 (bases 1 to 27)
Burke, D., Grinna, L., Baltaian, M., Horwitz, A. and Theofan, G. Stable bactericidal/permeabilityincreasing protein products and pharmaceutical compositions containing the same Patent: EP 1013760-8 28-JUN-2000;
XOMA TECHNOLOGY LT (BM)
Location/Qualifiers
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Grinna,L.S.
Methods for the preparation of endotoxin-binding proteins
Patent: US 5439807-A 17 08-AUG-1995;
Location/Qualifiers
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Sequence 17 from patent US 5439807.
1113573.1 GI:996640
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Sequence 8 from patent US 5447913.
114327
114327.1 GI:997342
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/db_xref="taxon:32644"
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    Sequence 8 from Patent EP1013760.
AX030652
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1 (bases 1 to 27)
Ammons, W.S. and Little, R.G.
                                          AX030652.1 GI:10278178
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Best Local Similarity 100.
Matches 12; Conservative
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1 (bases 1 to 33)
Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trikha, M. and Honn, K.V.
Antibodies specific for soluble truncated integrins
Patent: US 6218514-A 9 17-APR-2001;
Location/Qualifiers
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                         synthetic construct.

synthetic construct
artificial sequence.

1 (bases 1 to 30)
Shimkets,R.A., Lichenstein,H. and Boldog,F.L.
Proteins and polynucleotides encoded thereby
Proteins and polynucleotides encoded thereby
Proteins (027277-A 24 19-APR-2001;
Curagen Corporation (US)
Location/Qualifiers
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100.0%; Pred. No. 2.3e+04;
iive 0; Mismatches 0;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer 10354784 Rev"
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Sequence 4 from patent US 5869337.
AR034283
AR034283.1 GI:5949888
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10 c 9 g
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Sequence 9 from patent US 6:
AR146549
 AX179323.1 GI:14598994
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Patent: US 5703038-A 8 30-DEC-1997;
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Eckner, F., Swen, M. and Livingston, D.
Nucleic acid encoding transcription factor p300 and uses of p300
Patent: US 5658784-A 13 19-AUG-1997;
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162302,1 GI:2480250
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Sequence 8 from patent US 5703038.
187071
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Sequence 24 from Patent WO0127277.
AX179323
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Ammons, W. Steve and Little, R.G.
                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 100.
Matches 12; Conservative
Conservative
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                                         10 GCCACCATGGCC 21
                          1 GCCACCATGGCC 12
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JOURNAL Patent: US 5869337-A 4 09-FEB-1999;
FEATURES Location/Qualifiers
1. .33
//oranlsm="unknown" 3 t
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BASE COUNT ORIGIN

0; Gaps Query Match 100.0%; Score 12; DB 6; Length 33; Best Local Similarity 100.0%; Pred. No. 2.2e+04; Matches 12; Conservative 0; Mismatches 0; Indels

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οy qq Search completed: January 17, 2002, 11:49:54 Job time: 17206 sec

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1 GCCTTAAGGGC 11
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Matches 11; Conserv
US-09-258-377-22
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Sequence 18, Appl
Sequence 18, Appl
Sequence 7, Appli
Sequence 7, Appli
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  (without alignments)
  11.255 Million cell updates/sec
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5, Appl
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Sequence 45,
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Sequence 19,
Sequence 19,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-283-377-22

US-08-384-305-23

US-09-28-377-31

US-08-873-479-19

US-08-873-479-19

US-08-873-479-18

US-08-972-661A-18

US-08-972-661A-18

US-09-031-442A-7

US-09-031-442A-9

US-08-873-479-46

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US-08-972-661A-27
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  January 17, 2002, 11:52:06
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GENERAL INFORMATION:
APPLICANT: Michael D. Thomas
APPLICANT: Michael D. Thomas
APPLICANT: Minberly M. Brown
TITLE OF INVENTION: Polypeptides Having Pectin
TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same
FILE REFERENCE: 5952.000-US
CURRENT APPLICATION NUMBER: US/09/384,305
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 17
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                                                 Sequence 21, Appl Sequence 22, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 4, Appli Sequence 4, Appli Sequence 13, Appl Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli
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Patent No. 5256558
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Fatent No. 6255076
GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a TITLE OF INVENTION: Bacillus Cell
FILE REFERENCE: 5455.200-US
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1998-02-26
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 11; DB 4; Length 17; llarity 100.0%; Pred. No. 80; Conservative 0; Mismatches 0; Indels
US-09-258-377-3
US-09-384-305-20
US-09-384-305-22
US-09-258-377-25
US-09-258-377-25
US-09-048-052-5
US-09-160-246-5
US-08-110-416A-12
US-08-110-416A-12
US-08-110-416A-12
US-08-110-416A-12
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US-08-110-416A-12
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US-09-160-246-9
US-09-160-246-13
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0; Mismatches
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                                                                                                                                        TYPE: DNA ORGANISM: Bacillus subtilis US-09-384-305-23
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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CRGANISM: Bacillus
US-09-258-377-28
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US-09-258-377-28
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                     4; Length 17;
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATTON:
NAME: Agris, Cheryl H
REGISTRATION NUMBER: 34,086
REGISTRATION NUMBER: 34,086
REGISTRATION NUMBER: 5251.000-US
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US-09-384.305-23
US-09-384.305-33
Sequence 23, Application US/09384305
Sequence 23, Application US/09384305
Sequence 23, Application US/09384305
SERERAL INFORMATION:
APPLICANT: Michael D. Thomas
APPLICANT: Kimberly M. Brown
TITLE OF INVENTION: Polypeptides Having Pectin
                                                                                                               Mismatches
                                                                         100.0%; Score 11; 100.0%; Pred. No. 8
                                                                                                                                                                                                                                                                               Sequence 39, Application US/08873479 Patent No. 5891701
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
                                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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2 gccttaagggc 12
; ORGANISM: Bacillus
US-09-258-377-22
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US-08-873-479-39
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TITLE OF INVENTION: Acetylesterase Activity And Nucleic Acids Encoding Same File Reference: 5952.000-US CURRENT APPLICATION NUMBER: US/09/384,305 CURRENT FILING DATE: 1999-08-26 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 23 LENGTH: 33
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GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacilius Cell
FILE REFERENCE: 5455.200-US
CURRENT APPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/031,442
SERVILER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide in a TITLE OF INVENTION: Bacillus Cell;
FILE REFERENCE: 5455.200-US;
CURRENT RAPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/031,442
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASELED FOR Windows Version 3.0
SEQ ID NO 28
SEQ ID NO 28
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85;
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Sequence 18, Application US/08873479 Patent No. 5891701 GENERAL INFORMATION:
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"...ordTFR: IBM COMPATIBLE
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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                                                                                                                                   STREET: 400 CTTY: New York
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US-08-972-661A-19
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COUNTRY:
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                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
                                                                                                         DB 4; Length 33;
85;
                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
SOFTWARE: PastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-10N-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AGYIS, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                            0; Mismatches
                                                                                                         100.0%; Score 11; 100.0%; Pred. No.
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US-08-972-661A-19
Sequence 19, Application US/08972661A
Patent No. 5958728
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 11; Conserv
                ; TYPE: DNA
; ORGANISM: Bacillus
US-09-258-377-31
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US-08-873-479-19
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LENGTH: 33
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587280 No. 5958728disk Of No. 5958728th America, Inc.
STREET: 405 Lexington Avenue - 64th F1.
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APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58917010 No. 5891701disk of No. 5891701th America
STREET: 405 Lexington Avenue
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APPLICANT: Sternberg, David
APPLICANT: Adams, Lee F.
APPLICANT: Brown, Stephen
TITLE OF INVENTION: Method For Producing Polypeptides
TITLE OF INVENTION: In Mutants Of Bacillus Cells
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APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,661A
FILING DATE: 18-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Starnes, Robert L
REGISTRATION NUMBER: 41,324
REFERENCE/DOCKET NUMBER: 5111.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEPAX: 212-878-9655
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ADDRESSEE: No. 59553100 No. 5955310disk of No. 5955310th America, Inc. STREET: 405 Lexington Avenue CITY: New York
                                                                                                       Sequence 7, Application US/09031442A
Patent No. 5955310
GENERAL INFORMATION:
APPLICANT: Widner, William
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: Methods For Producing A Polypeptide
TITLE OF INVENTION: In A Bacillus Cell
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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FR: 5455.000-US
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CURRENT APPLICATION NUMBER: US/09/258,377
CURRENT FILING DATE: 1999-02-26
BARLIER APPLICATION NUMBER: 09/031,442
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ATORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5455
TELECHONE: 212.867-0123
TELEPHONE: 212.867-0123
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SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
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Best Local Similarity 100.
Matches 11; Conservative
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                  22 GCCTTAAGGGC 12
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US-09-258-377-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,661A
FILING DATE: 18-NOV-1997
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Pred. No. 85;
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New York
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11arity 100.0%; Pred. No. 4
Conservative 0; Mismatch
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                                    5251.000-US
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US-08-972-661A-18/c
: Sequence 18, Application US/08972661A
; Patent No. 5958728
                                                                                                                                                                                                                                                                                                                 6
 NAME: Agris, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 525
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 521
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Starnes, Robert L
REGISTRATION NUMBER: 41,324
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100.0%;
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APPLICANT: Sternberg, David
APPLICANT: Adams, Lee F.
APPLICANT: Brown, Stephen
                                                                                                                         INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.

Matches 11; Conservative
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MEDIUM TYPE: Diskette
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EDNESS: single
                                                                                   TELEFAX: 212-878-9655
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Best Local Similarity
Matches 11; Conserv
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US-08-873-479-18
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APPLICANT: Widner, William
APPLICANT: Sloma, Alan
APPLICANT: Homas, Michael D.
TITLE OF INVENTION: Methods For Producing A polypeptide In a
TITLE OF INVENTION: Bacillus Cell
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Length 37;

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APPLICANT: Sloma, Alan
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
APPLICANT: Adams, Lee F.
APPLICANT: Brown, Lee F.
TITLE OF INVENTION: Method For Producing Polypeptides
TITLE OF INVENTION: In Mutants Of Bacillus Cells
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587280 No. 5958728disk Of No. 5958728th America, Inc.
STREET: 405 Lexington Avenue - 64th Fl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 58917010 No. 5891701disk of No. 5891701th America
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Having Protease Activity
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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NAME: Starnes, Robert L
REGISTRATION NUMBER: 41,324
REFERENCE/DOCKET NUMBER: 5111.200-US
TELECOMMUNICATION INFORMATION:
TELEBRONE: 212-878-9652
TELEFAX: 212-878-9655
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Sequence 37, Application US/08873479
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Having Protease
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
Sequence 32, Application US/08972661A Patent No. 5958728 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 405 Lexington Avenue CITY: New York
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100.0%;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity 100.
Matches 11; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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38 GCCTTAAGGGC 28
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US-08-972-661A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF INVENTION: Having Protease Activity NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFTCATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: AGIS, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 86;
Mismatches
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                     NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-873-479-46/c
Sequence 46, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
APPLICANT: Lynne, Christianson
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Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
    EARLIER FILING DATE: 1998-02-26
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100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 212-878-9655
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US-08-873-479-46
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(without alignments)
358.829 Million cell updates/sec
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1 GCCTTAAGGGCCATATGGTG......GGTGTCCTCTATAATATTAT
4.5
Compugen Ltd.
                                                                                                                                                                                                                                             Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      1472140 seqs, 8248589755 residues
 GenCore version
Copyright (c) 1993 - 2000
                                                                          January 17, 2002, 07:03:08
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AR102855 Sequence 3
AR102885 Sequence
AR108064 Sequence
AR134712 Sequence
AR1343B Human growt
A18662 Synthetic c
A20119 Hybrid insu
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AF67197 Cloning v 141411 Sequence 5 AR119909 Sequence AF239248 Eukaryoti AF237583 Homo sapi K00470 Homo sapien M15894 Human chori AC040958 Homo sapi AC015651 Homo sapi 102858 Sequence 4 AF237586 Homo sapi Z32693 E.coli pT7h Z32691 E.coli (HM1 AF110644 HOMO Sapi E00009 MRNA coding J00289 Homo sapien U02293 Macaca mula AF237584 Homo sapi Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1964) V00520 Human germ 2 (bases 1 to 1964)
Adelman,J.P., Hayflick,J.S., Vasser,M. and Seeburg,P.H.
In vitro deletional mutagenesis for bacterial production of the DeNoto, F.M., Moore, D.D. and Goodman, H.M.

Human growth hormone DNA sequence and mRNA structure: possible alternative splicing
Nucleic Acids Res. 9 (15), 3719-3730 (1981)

82014939 complementary DNA; germ line; growth hormone; signal peptide HSGROWZ 1964 bp DNA PRI 10-FEB-1 Human germ line gene for growth hormone (presomatotropin). V00520 J00148 K00612 V00520.1 GI:31906 ALIGNMENTS 141411 AR119909 AF239248 AF237583 AF239250 AF067196 AF067197 AF239247 AF239251 **PVPHM3BL** AF369966 HSA7670 AX060703 HUMGHCSA AC040958 AC084858 AF237585 PVPHM3 AF396260 AC015651 I02858 AC040958 AF237586 AR108064 HSGROW2 A18663 A20119 A20120 DB Length 4775 4912 5646 9274 66495 8451 2660 2660 2740 159128 191583 1125 2033 831 2086 2086 2086 22687 3141 3141 3141 4495 4650 4665 4665 1944 6776 Homo sapiens Query DEFINITION ACCESSION ORGANISM AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE REFERENCE RESULT HSGROW2 Š.

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Gaps

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Length 2771;

16-MAY-2001

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FEATURES COMMENT

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BASE COUNT ORIGIN

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Expression vector pCMV4 artificial sequence; vectors.

1 (bases I to 487).

Andersson, S., Davis, D.L., Dahlback, H., Jornvall, H. and Russell, D.W. Cloning, structure, and expression of the mitochondrial cytochrome p-450 sterol 26-hydroxylase, a bile acid biosynthetic enzyme 99255259 and Chem. 264 (14), 8222-8229 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 4874)
Addresson, S., Davis,D.L., Dahlback,H., Jornvall,H. and Russell,D.W.
Direct Submission
Submitted (25-FEB-2000) Molecular Genetics, University of Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4324 AGIGCCITCTCCIGGCCIIGGAAGIIGCCACICCAGIGCCCACCAGCCIIGICCIAAIAAA 4383
                                                                                                                                                      2177 AGIGCCTCTCCTGGCCTTGGAAGTTGCCACTCCAGTGCCCACCACCAGCCTTGTCCTAATAAA 2236
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King, D. and Schneider, G.B.
Erythropoletin-inducible, erythroid-specific DNA construct
Patent: US 6153427-A 1 28 NOV-2000;
Location/Qualifiers
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Eukaryotic expression vector pCMV4, complete sequence.
AF239248.1 GI:7542545
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Pred. No. 7.3e-21;
0; Mismatches 1;
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Pred. No. 7.5e-21;
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 /organism="unknown"
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Matches 106; Conservative
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RLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELL
RISLLLIQSWLEPVQFLRSVFANSLYYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPR
TGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKDMDKVETFLRIYQCRSYEGSCGF"
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/db.xref="taxon:9606"
(274.275) ..1905
join((274.275) ..344,601. .761,971. .1090,1184. .1348,
1602. ..1905 ..344
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                                                This entry was previously called <HSGROWZ1>.
See <HSGROW1> for mRNA sequence (with some differences).
Location/Qualifiers
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20,000-dalton form of human pituitary growth hormone DNA 2 (3), 183-193 (1983) 84057143
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Pred. No. 7.6e-21;
0; Mismatches 1
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/product="growth hormone"
/protein_id="CAA23779.1"
/db_xref="G1:312406"
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LTSGVHTFPAVLQSSGLXSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHYCPPCPAPELLGGPSVFLFPPRRKDTLAISRTPENTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQY NTTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKQOPREPQYYTTPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESKGQPENNYKTT
PPVLDSDGSFFLXSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1827)
Vidarsson, G., van der Pol, W.L., van den Elsen, J.M.H., Vile, H.,
Jansen, M., Dulis, J., Morton, H.C., Boel, E., Daha, M.R., Corthesy, B.
and van de Winkel, J.G., J.
Activity of Human IgG and IgA Subclasses in Immune Defense Against
Neisseria meningitidis Serogroup B
J. Immunol. 166 (10), 6250-6256 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University
6, Utrecht 3584
                                                                                                                                                                                                                                                         1055 AGTGCCTCTCCTGGCCTTGGAAGTTGCCACTCCAGTGCCCACCACCCTTGTCCTAATAAA 1114
Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235, USA
Location/Qualifiers
                                                                                                                                                                                                                                        121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              AF237583 1827 bp DNA PRI 11-MAY-2001
Homo sapiens recombinant IgG1 heavy chain gene, partial cds.
AF237583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(<1. .294,686. .730,849. .1178,1276. .>1598)
/product="recombinant IgG1 heavy chain"
join(<1. .294,686. .730,849. .1178,1276. .1598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1827)
Vidarsson,G., Jansen,M., Boel,E. and van de Winkel,J.G.J.
Vidarsson,G., Jansen,M., Boel,E. and van de Winkel,J.G.J.
Direct Submission
Submitted (22-FEB-2000) Department of Immunology, Univers
Medical Center Utrecht, Rm. KC.02-085.2, Lundlaan 6, Utree
EA, The Netherlands
                                                                                                                                                                        Length 4874;
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0
                                                                                                                                                                                                                                                                                                                           Score 105.4; DB 12; Length
Pred. No. 7.3e-21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                         181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="recombinant igG1 heavy chain"
/protein_id="AAG00909.1"
/db_xref="GI:9857753"
                                                               /organism="Expression vector
/db_xref="taxon:120119"
1237 c 1170 g 1302 t
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/db_xref="taxon:9606" .
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99.1%;
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1276. 1598
/note="CH3"
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nes 106;
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Best Local 3
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SOURCE
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1 (bases 1 to 2086)
Newgard, C.B., Normington, K.D., Clark, S.A., Thigpen, A.E., Quaade, C.
                                                                                                                                                                                                                    1638 TGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCACCAGCATTGTCCTAATAAAAT 1697
                                                                                                                                                    TGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAAT 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant expression of proteins from secretory cell lines Patent: US 6087129-A 9 11-JUL-2000; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth hormone varient genes
                                                                Length 1827;
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                                                                Score 98; DB 9; Pred. No. 1.2e-18; 0; Mismatches 35
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Method for cloning human growth horn
Patent: US 4446235-A 3 01-MAY-1984;
 316
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Sequence 9 from patent US 6087129.
AR102885
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Sequence 3 from Patent US 4446235.
102857
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South San Francisco, CA
Location/Qualifiers
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231 c 219 g
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621
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VERSION
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1 (bases 1 to 2086)

Newgard.C.B., Halban,P., Normington,K.D., Clark,S.A., Thigpen,A.E., Quaade,C., Kruse,F. and McGarry,D.
Recombinant expression of proteins from secretory cell lines
Patent: US 6110707-A 9 29-AUG-2000;

Location/Qualifiers
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Newgard, C.B., Halban, P., Normington, K.D., Clark, S.A., Thigpen, A.E., Quaade, C. and Kruse, F. Recombinant expression of proteins from secretory cell lines
Recombinant expression of proteins from secretory cell lines
Patent: US 6194176-A 9 27-FEB-2001;
Location/Qualifiers
1. 2086
                                                                                                                                   121 AGTGCCTCCTCGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
                                                                                                Gaps
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Pred. No. 4.8e-18;
0; Mismatches 0; Indels
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                                                                42.3%; Score 96; DB 6; 99.1%; Pred. No. 4.8e-18; ive 0; Mismatches 0
                466
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US 6110707.
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AR134712
AR134712.1 GI:14123617
/organism="unknown"
456 a 604 c 560 g
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604 c 560 g
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604 c 560 g
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Sequence 9 from patent US
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ilarity 99.1%;
Conservative 0
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Best Local Similarity 99.1:
Matches 107; Conservative
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Best Local Similarity
Matches 107; Conserv
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             BASE COUNT
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JOURNAL
FEATURES
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AR108064
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AR134712
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KEYWORDS
SOURCE
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.988,1196. .1315,1409. .1573,1827. .2024)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLHQLAFDTYQEFEBAYIPKEQKYSFLQNPQTSLCFSBSIPTPSNREBTQQKSNLELL
RISLLLIQSWLEPYQFLRSVFANSLVYGASDSNVYDLLKDLEGIQTLMGRLEDGSPR
TGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MATGSRTSLLLAFGLLCLPWLQEGSAFPTIPLSRLFDNAMLRAH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone DNA 1 (3), 239-249 (1982) 83182010
                                                                                        AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                           M13438.1 GI:183156
Alu repeat; growth hormone; hormone; repeat region.
Homo sapiens (clone: HGH-N.) (tissue library: Lawn et al.) DNA.
Homo sapiens
                                                 Gaps
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      Length 2086;
                                                                                                                                                                       HUMAN GES7 bp DNA PRI HUMAN Growth hormone gene (HGH-N), complete cds. M13438.1 GI:1837FK
    Score 96; DB 6; I
Pred. No. 4.8e-18;
0; Mismatches 0;
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'protein_id="AAA98618.1"
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/map="17q21-qter"
497. :568
/gene="GH-N"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HGH-N."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
1 (bases 1 to 2657)
Seeburg, P.H.
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join(ff.
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/gene="GH-N"
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prim_transcript 497. .2129
/gene="GH-N"
/note="HGH-N mRNA"
gene 497. .2129
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Query Match
Best Local Similarity 99.1%;
Matches 107; Conservative
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/product="growth hormone"

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NVYHLMWQEPKEPNGLIYLYEVSYRRYGDEELHLCVSRKHFALERGCRLRGLSPGNYS
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  EPYWPPDFRDLLGFMLFYKEAPYONVTEFDGODACGSNSWTVVDIDPPLRSNDPKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="polypeptide of extracellular domain of hybrid insulin/IGF-I receptor"
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3000...3059
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insulin/IGF-I receptor"
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3060. .3141
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99.1%; Pred. No. 4.7e-18;
iive 0; Mismatches 0
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/transl_table=11
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VDRPFCANTLSAESSDSEGFYTHDGECMQECPSGFTRNSSNLLCTPCLGPCPRVCHLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKSGSGGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2057 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 2116
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Synthetic cDNA sequence for hybrid insulin/IGF-I receptor.
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4.7e-18;
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Pred. No. 4.7e-
0; Mismatches
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/rpt_family="Alu"
598 a 741 c 734 g 5i
1 bp upstream of EcoRI site.
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99.1%;
                                                                                                          1316. 1408
/gene="GH-N"
                                                                                                                                                                                                                             1574. .1826
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                                                                                                                                                                                                                                                                                     1827. .2129
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synthetic construct
artificial sequence.
1 (bases 1 to 3141)
                                                    1196. .1315
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                                                                                                                                                                    1409. .1573
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                                                                                          /number=3
1316. .140
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                                      'number=2
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Best Local Similarity 99.1
Matches 107; Conservative
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Length 3141;

22-JUL-2001

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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGFKELTAFLHNMGDHVTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 4495)
Garafaxy.A.D. III.
Direct Submission
Submitted (16-APR-2001) Technical Services, Stratagene, 11011 N.
Torrey Pines Rd., La Jolla, CA 92037, USA
1.0cation/Qualifiers
1.4495
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Pred. No. 4.7e-18;
0; Mismatches 0; Indels
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Cloning vector pCMV-MCS
Cloning vector pCMV-MCS
1 (base1 lsequence; vectors.
1 (base3 lto 4495)
Grafeky,A.J. III.
Unpublished
Unpublished
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/note="similar to beta-globin intron"
1178. .1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1844..2701)
/note="CoLD1 origin"
complement(2711..357)
/note="confers ampicillin resistance"
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1. 670
/note="CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF369966 4495 bp DNA circular SYN
Cloning vector pCMV-MCS, complete sequence.
                                                                                                                                                                      /organism="synthetic construct"
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863 c 892 g 717 t
                                                                                                                               14-NOV-1991;
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                                                                                                   A HYBRID CELLULAR RECEPTOR
Patent: WO 9117252-A 16 14
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/note="hGH/poly A"
complement(1844. .2
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                                                                                                                                                                                                                                                                 Query Match 42.3%;
Best Local Similarity 99.1%;
Matches 107; Conservative
                                                              artificial sequence.
1 (bases 1 to 3141)
                               synthetic construct
                                              synthetic construct
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/note="MCS"
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 Synthetic cDNA sequence for hybrid insulin/IGF-I receptor. A18663
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99.1%; Pred. No. 4.7e-18;
tive 0; Mismatches 0; Indels
                                                                                                                                         WAWMALIAN CELLS EXPRESSING A HYBRID RECEPTOR
Patent: WO 9117253-A 15 14-NOV-1991;
Location/Qualifiers
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                                                                                                                                                                                                                construct"
                                                                                                                                                                                                                                                                                                  42.3%; Score 96; DB 99.1%; Pred. No. 4.7e tive 0; Mismatches
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Location/Qualifiers
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Hybrid insulin/IGF-I receptor mRNA.
A20120.1 GI:578998
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/organism="synthetic cc
/db_xref="taxon:32630"
863 c 892 g 7
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/db_xref="taxon:32630"
892 c 863 q
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Hybrid insulin/IGF-I r.

A20119

A20119.1 GI:583286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct.
synthetic construct
artificial sequence.
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                                                                                              artificial sequence.
1 (bases 1 to 3141)
                                                             synthetic construct.
                               A18663.1 GI:512264
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Matches 107; Conservative
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Best Local Similarity 99.17
Matches 107; Conservative
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DEFINITION
                                                                             ORGANISM
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ACCESSION
VERSION
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13

RESULT A20119

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ACCESSION

KEYWORDS

SOURCE

VERSION

BASE COUNT

ORIGIN

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REFERENCE AUTHORS

JOURNAL FEATURES

TITLE

RESULT 14 A20120/c

Locus

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DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQOLIDWMEADKVAGPL
LRGALPAGNFTADKSGAGERGSRGIIAALGPDGKPSRIVVITTGSQATWDERNRQIA
EIGASLIKHWA
COMPLEMENt(3952. .4413)

BASE COUNT 1124 a 1117 c 1101 g 1153 t

ONLGIN

Query Match 42.3%; Score 96; DB 12; Length 4495;
Best Local Similarity 99.1%; Pred. No. 4.6e-18;
Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db

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Search completed: January 17, 2002, 11:48:13 Job time: 17105 sec

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Human secreted pro Not1/Sall psk-GHRH Secretory cell DNA Human growth hormo Human growth hormo

Human growth hormo

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Extracellular doma Soluble human insu Hybrid human insu Hybrid human insu Hybrid human insul plasmid pIF0031 co plasmid pIF0032 lo Actual sequence of Plasmid pIG0552 up Expected sequence Plasmid pIN143 co Nucleotide sequence Beta-domain delete HERZ transgene pla Vector VIII protei Cosmid CV014 conta plasmid phmnyve40RF Sequence of gene f

Human cancer speci Met-des(F1-P2-T3-I Met-des(F1-P2-T3-I Met-des(Phel-Pro2-Met-des(Phel-Pro2-Met-des(Phel-Pro2) Met-des(Phel-Pro2) Met-des(Phel-Pro2)

Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database

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Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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 97WO-US14306.
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                                              Welson EL, Nelson PJ;
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Homo sapiens.
Synthetic.
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 RESULT
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Humanised vector s
Humanised vector p
Rat Fabpl gut-spec
                                                                                                                         (without alignments) 324.430 Million cell updates/sec
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                                                                                                                                                                                              1 GCCTTAAGGGCCATATGGTG......GGTGTCCTCTATAATATAT 227
                                                                                                       ; Search time 599.86 Seconds
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           930621 seqs, 428662619 residues
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                                                                                                      January 17, 2002, 07:06:53
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Listing first 45 summaries
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AAV21733
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AAV21724
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AAV31727
AAV33343
                                                                       nucleic - nucleic search, using sw model
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AAV21723
                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Score

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AAV21732
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                                                                                                                                                                                                                                                                    0;
This DNA sequence comprises a combined 3' splice sequence and polyA tail sequence derived from human gene sequences. Novel humanised vectors of the invention (see AAT21724, AAT21727 and AAT21732-34) comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and an acceptance site which accepts cDNA products from RT-PCR cloning. They may also include human-derived splice-polyA sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                      61 AGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGATGAGTAGTG 120
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors
                                                                                                                                                                                                                                                                                            1 GCCTTAAGGGCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGGGATGGGGAGACCTGT 60
                                                                                                                      an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or
                                                                                                                                                                       peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
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                                                                                                                                                                                                                                            Length 227;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 attaagttgcatcattttgtctgactaggtgtcctctataatattat 227
                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTAT
                                                                                                                                                                                                                                           Query Match 100.0%; Score 227; DB 19; Best Local Similarity 100.0%; Pred. No. 1.4e-62; Matches 227; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          Sequence 227 BP; 47 A; 64 C; 60 G; 56 T; 0 other;
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18..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised vector splice polyA signal sequence.
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121..228
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/number= 4
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/*tag= d
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning. They may also include the splice-polyA signal and an acceptance site which accepts cDNA products from RT-PCR cloning. They may also include the splice-polyA signal RT-PCR sequence. After processing of mRNA, intron 31s exclised, and the sequence contains duplicate stop codons in 2 reading frames.

A 3rd reading frame stop codon can be obtained by mutagenising the internal ribosomal entry site (RRES). The vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences, and selectively elicit immune responses to the target sequences with little or no immune response to the target sequences with little or no immune capposes as intracellular polypeptides and are appropriately presented on antigen presenting cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                        _{\mbox{\scriptsize Humman}} sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCTTAAGGGCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGGAT-GGGGAGACCTG
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0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.4%; Score 214.4; DB 19; 99.1%; Pred. No. 1.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 228 BP; 47 A; 63 C; 62 G; 56 T; 0 other;
                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                            Example 1; Page 27; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV21732 standard; cDNA; 1547
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Chimeric - Escherichia coli.
Synthetic.
   96US-0023931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised vector pITL-A.
                                                                                                                      Nelson EL, Nelson PJ;
                                                                                                                                                                          WPI; 1998-159552/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
14-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998
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AAV21733 standard; cDNA; 1807 BP.

AAV21733 RESULT

(first entry)

17-AUG-1998

AAV21733;

Humanised vector pITL-1.

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in mammalian target tissue and cells and a sequence acceptance site (see AAV21735-36) which accepts CDNA products from RT-PCR cloning. They also contain minimal non-human components, such as a replication origin (see AAV21715) and selectable marker gene (see AAV21717-18) that are necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 TAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGATGAGTAGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCCTTAAGGGCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGGAT-GGGGAGACCTG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pITL-A comprises a base vector for novel humanised bolynucleotide vectors. The vector in Escherichia coll DH 10-beta/P3 is deposited as ATCC 98401. Novel vectors comprise a human-derived promoter or mammalian homologue which is functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.4%; Score 214.4; DB 19; Length 1547; Best Local Similarity 99.1%; Pred. No. 2.8e-58; Matches 226; Conservative 0; Mismatches 1; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1547 BP; 344 A; 408 C; 425 G; 370 T; 0 other;
                                                                                                   /*tag= d
/note= "ColE1 origin of replication"
1311..1547
                                                                                                                                                    /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 56-57; 125pp; English.
               Location/Qualifiers
                                               /*tag= c
/note= "SupF gene"
                                                                                                                                                                                                                                                                       97WO-US14306.
                                                                                                                                                                                                                                                                                                       96US-0023931
                                                                               686..1292
                                 72..680
                                                                                                                                                                                                                                                                                                                                                                          Nelson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-159552/14.
                                                                                   misc_feature
                                                                                                                                                                                                                                                                     14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                          Nelson EL,
                                                                                                                                    promoter
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Plasmid pITL-1 comprises a base vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH 10-beta/73 is deposited as ATCC 98400. Novel vectors comprise a human derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site (see AAV21735-36) which accepts cDNA products from RT-PCR cloning. They also contain minimal non-human components, such as a replication origin (see AAV21717) and selectable marker gene (see AAV21717-18) that are necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1807 BP; 419 A; 463 C; 492 G; 433 T; 0 other;
                                                                                                                                                                                                           Vector; vaccine; tumour; antigen; plasmid pITL-1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
/note= "ColE1 origin of replication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "RANTES promoter"
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472..680
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/note= "SupF gene"
686..1292
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                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
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Gaps

Ouery Match 94.4%; Score 214.4; DB 19; Length 1807; Best Local Similarity 99.1%; Pred. No. 3e-58; Matches 226; Conservative 0; Mismatches 1; Indels 1;

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14-AUG-1997;
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                                                                                                                                Query Match
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                                                    292 tagtcagagcccccgggcagcacaggccaatgcccgtccttcccctgcaggatgagtagt 351
                                                                                           352 gagtgeeteteetggeeetggaagttgeeaeteeagtgeeeaecageettgteetaataa 411
29
                232 gccttaagggccatatggtgagtggatgccttgaccccaggcggggatggggggagacctg 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pITL-1 GFP comprises base vector pITL-1 (see AAV21733) and a humanised green fluorescent protein (GFP) reporter sequence (see AAV21725). Novel humanised vectors comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which
GCCTTAAGGGCCATATGGTGGATCCCTTGACCCCAGGCGGGAT-GGGGAGACCTG
                                   TAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGATGAGTAGT
                                             180 AATTAAGTTGCATCATTTGTCTGACTAGGTGTCCTCTATAATATTAT 227
                                                                                                                                                                                                                                                    tumour; antigen; plasmid pITL-1 GFP;
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/note= "ColE1 origin of replication"
                                                                                                                                                                                                                                                                                                                                                     /product= green fluorescent protein 973..1181
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/note= "RANTES promoter'
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20..734
/*tag= a
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/note= "SupF gene'
                                                                                                                                                                           AAV21734 standard; cDNA; 2308
                                                                                                                                                                                                                                                          green fluorescent protein; ds
                                                                                                                                                                                                                                                                                       - Escherichia coli.
- Aequorea victoria
                                                                                                                                                                                                                                 Humanised vector pITL-1 GFP
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/*tag= d
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                                                                                                                                                                                                                                                    Vector; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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Chimeric
                                                                                                                                                                                             AAV21734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
accepts cDNA products from RT-PCR cloning. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately
                                                                                                                                                                                                                                                                                                                                                                                  94.4%; Score 214.4; DB 19; Length 2308; 99.1%; Pred. No. 3.3e-58;
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/*tag= b
/note= "combined splice and polyA sequences"
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/note= "ColE1 origin of replication"
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"stuffer sequence"
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/note= "RANTES promoter"
                                                                                                                                                                                                                                                    presented on antigen presenting cells.
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/note= "SupF gene"
712..1164
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Chimeric - Escherichia coli
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Matches 226; Conservative
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Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
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                                                                                                                                                              polyA_site
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                              promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 tagtcagagcccccgggcagcacaggccaatgcccgtccttcccctgcagtgagtagtga 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 ctgcccgggtgggatccctgtgacccctccccagtgcctctcctggccctggaagttgcc 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised polynucleotide vectors – comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTAAGGGCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGGAT-GGGGAGACCTG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 ------GATGAGTAGTGAGTGCCTCTCCTGGCCTGGAAGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 ACTCCAGTGCCCACCAGCCTTGTCCTAATAAATTAAGTTGCATCATTTTGTCTGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19; Length 1425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 160.6; DB 19; Length
Pred. No. 3.1e-41;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu; human; HER-2/neu; C-erbB-2; breast cancer; ds.
                                                                                                                                                                                                                                                    Plasmid pITL comprises a base vector for novel humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1425 BP; 325 A; 381 C; 404 G; 315 T; 0 other;
                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 presented on antigen presenting cells.
                                                                                                                                                                                                               Claim 14; Page 29-30; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV21727 standard; cDNA; 2125 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised vector pITL-hHER/neu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 gtgtcctctataatattat 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTCCTCTATAATATAT 227
                96US-0023931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                      Nelson PJ;
                                                                                                                          WPI; 1998-159552/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
Matches 218; Conserv
                14-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1998
                                                                                        Welson EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV21727;
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ID AAV2
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AC AAV2
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KW Vect
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922 gccttaagggccatatggtgagtggatgccttgaccccaggcggggatgggggagacctg 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GATGAGTAGTGGGCCTCCTGGCCTGGAAGTTGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a human HER. 2/neu nucleic sequence. PITL-HEREZ/neu was used to evaluate the toxicity of anti-tumour vaccination in rats, and in phase I and phase II trials to evaluate polyuclectide vaccination in advanced breast cancer. Novel humanised vectors, which can be based on PITL, comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells but are capable of extended stable expression of the target sequence, generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the carget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pITL-hHER2/neu comprises base vector pITL (see AAV21724) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTTAAGGGCCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGGAT-GGGGAGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 2125;
                                                                                                                                                                   /*tag= b
/note= "combined splice and polyA sequences"
1195..1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.7%; Score 160.6; DB 19; Length
84.2%; Pred. No. 3.7e-41;
ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2125 BP; 449 A; 650 C; 598 G; 428 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "ColE1 origin of replication"
                                                                   ′*tag= a
'product= human HER-2/neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 41-42; 125pp; English.
Location/Qualifiers
13..921
                                                                                                                                                                                                                                                                           /*tag= c
/note= "SupF gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US14306
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Best Local Similarity 84.2
Matches 218; Conservative
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Matches
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1042 ctgcccgggtgggatccctgtgaccctccccagtgcctctcctggcctggaagttgcc 1101
                 Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humanised green fluorescent protein (GFP) reporter sequence (see AAV21725). Novel humanised vectors comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which excepts cDNA products from RT-PCR cloning. pITL-GFP was used to examine the kinetics of expression of a reporter sequence from such vectors in an animal model (Fisher 344 rats). Toxicity from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pITL-GFP comprises base vector pITL (see AAV21724) and a
                                                                                                                                                                                                                                                                                          /*tag= b
/note= "combined splice and polyA sequences"
981..1187
                                                                                                                                                                                                                                                                                                                                                    replication"
                                                                                                                                                                                                                                                                          /product= green fluorescent protein 720..967
                                                                                                                                                                               Vector; vaccine; tumour; antigen; plasmid pITLGFP;
                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                                                                                                                    origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 33-34; 125pp; English.
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "SupF gene"
                                                                                                              BP
                                                                                                             AAV21726 standard; cDNA; 1911
                                                                                                                                                                                                                                                                                                                                                   /note= "ColE1
                                                             green fluorescent protein; ds
                                                                                                                                                                                                                       Chimeric - Aequorea victoria
                                                    209 GIGICCICIAIAATATIAT 227
                                                                                                                                                                                                        Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                    1198..1650
                                                                                                                                                                                                                                                                                                                                                             1663..1911
                                                                                                                                                               Humanised vector pITL-GFP.
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                                                                                                                                                                                                                                                         2..719
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-159552/14.
                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                              17-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998
                                                                                                                                                                                                                                                                                    polyA_site
                                                                                                                                                                                                                                  Synthetic
                                                                                                                              AAV21726;
                                                                                                                                                                                                                                                                                                                                                              promoter
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Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase; GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase; alpha 1.2 FT; alpha 1.34 FT; tissue specific promoter; rat liver fatty acid binding protein; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithellal cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 gagccatatggtgagtggatgcettgaccccaggcggggatgggggagacctgtagtcag 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAG------- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 -------GATGAGTAGTGAGTGCCTCTCCTGGCCTGGAAGTTGCCACTCCAG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 GGGCCATATGGTGAGTGGATCCCTTGACCCCAGGCGGGAT-GGGGAGACCTGTAGTCAG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                           stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and as such presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the human growth hormone (hGH) gene; it is desirable for cDNA coding for a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 TGCCCACCAGCCTTGTCCTAATAAATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCT
polynucleotide vaccination was examined. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "Corresponds to nucleotides -596 to +21 of
the rat liver fatty acid binding protein
gene"
620..2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    776 agececegggeageacaaggecaatgeeegteetteeeetgeagtgagtagtgactgeeeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Corresponds to nucleotides +3 to +2150 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Fabpl gut-specific promoter and human growth hormone exon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 1911 BP; 474 A; 514 C; 511 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 152; DB 19;
Pred. No. 1.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               67.0%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1997 (first entry)
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- Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..617
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 210; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Nucleotide sequence of HS2-betaglobin-hGH transgene.
                                                                                                                                                                                                                          Chimeric - Homo
Chimeric - Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-0CT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNE-) UNIV
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                                                                                                                                                                                                                                                                                                                                       US6153427-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells, the enzyme human GDP-L-fucose: beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta-D-N-acetylglucosamide 3/4 alpha-L-fucosyltransferase (also called alpha 1,3/4 FT). The enzyme is expressed under the control of a gut epithelial cell-specific promoter and Helicobacter pylori adheres to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The first 617 nucleotides of the present chimeric sequence encode the promoter from rat liver fatty acid binding protein (Fabpl) which can direct foreign gene expression to the pit cell inneage of the mouse gastric epithelium, to proliferating and non-proliferating cells in intestinal crypts, as well as to the four principal differentiated cell lineages along the crypt-to-villus axis coft the small intestine. The remainder of the chimeric sequence corresponds to exon 1 of the human growth hormone (NGH) gene, into which a sequence coding for a human fucosyltransferase (NET) can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inserted. No hGH will be produced because the initiator Met codon and the first translation stop codon will be from the hFT sequence and there is no ribosome re-entry sequence. The hGH exon 1 ensures efficient splicing of the transgene primary transcript, improves stability of the cytoplasmic hFT mRNA and allows transgene expression to be monitored by in situ hybridisation using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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fucosyltransferase to be inserted into exon 1 of the hGH gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Animal model for Helicobacter pylori infection - comprising transgenic mouse expressing human enzyme promoting intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.4%; Score 105.4; DB 18; Length 99.1%; Pred. No. 1.3e-23; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     digoxigenin-labelled hGH oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Columns 25-28; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC83268 standard; DNA; 4456
                                                                                                                                                                                                                                                             94US-0273411.
                                                                                                                                                                                                                                                                                                                                       94US-0273411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-258275/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                             11-JUL-1994;
                                                                                                             US5625124-A
                                                                                                                                                                                   29-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC83268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falk P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACB3268
ID AACB
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DT 16-M
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This invention relates to a DNA construct comprising an erythropictin-inducible sequence represented by the present sequence. The HS2-betaglobin-hGH transgene comprises the hypersensitive site (HS2) element from the human beta-globin locus control region, the juvenile beta globin promoter isolated from sheep, and the human growth hormone (MGH) gene. The transgene results in osteopathic activity, when used in gene therapy. The DNA construct is useful for the treatment of osteopaenias, such as osteoporosis.
Erythropoietin-inducible transgene; human; sheep; juvenile beta globin; human growth hormone; hGH; osteopathic; osteopaenia; osteoporosis; hypersensitive element; HS; locus control region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA construct comprising an erythropoietin-inducible sequence, an erythroid-specific enhancer sequence and coding sequence of interest useful for treating osteopenia, particularly osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCACCAGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human interleukin 2; IL-2; CMV promoter; cationic lipid; DOTMA; human growth hormone 3'-untranslated region; lipid cholestrol; gene therapy; tumour; helper T cell; fever; fluid retention; vascular leak syndrome; human growth hormone 3' UTR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 4456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4456 BP; 1238 A; 978 C; 1076 G; 1164 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human growth hormone 3' UTR/poly(A) signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 46.4%; Score 105.4; DB 22; Best Local Similarity 99.1%; Pred. No. 1.6e-23; Matches 106; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
81..86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Fig 1B; 19pp; English.
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                                                                                                                                                                                                                                                                                                        94US-0321686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                              sapiens.
aries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schneider GB, King D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-060092/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
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the present sequence represents a human growth hormone 3' UTR/poly(A) signal sequence. The invention provides a pIL0697 plasmid comprising of a CMV promoter/enhancer transcriptionally linked to a codon portinised human IL-2 coding sequence (AAV3342) and the present human growth hormone 3'-untranslated region/poly(A) signal. Also, a 5' UTR (AAV3344) may be present between the 3' of the promoter region and the 5' of the IL-2 coding region. The invention also provides a composition for delivery and expression of a human IL-2 coding sequence in mammals, comprising: (a) a cationic lipid e.g. DOTMA, a neutral co-lipid e.g. lipid cholestrol and (b) a plasmid as described above. The plasmid composition may be used in gene therapy, especially therapy of tumours, as IL-2 is involved in stimulating proliferation of helper 7 cells. The claimed antitumour effect of the above formulations does not only depend on the expression level of IL-2 but is also a function of the non-DNA formulation components, with the effect being greater than merely additive. Also, as administration of high doses of IL-2 than merely additive. Also, as administration of high doses of IL-2 to rectain results in significant toxicity-related side effects, e.g. fever, fluid retention and vascular leak syndrome, the present composition is claimed to avoid such problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCACCACCACTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV; promoter; growth hormone; untranslated region; UTR; mammal; disease;
                                                                                                                                                                                                                                                                                                                      Plasmid for expression of a human IL-2 coding sequence - and lipid/DNA delivery systems which have suitable positive/negative charge ratios and are useful in treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.3%; Score 96; DB 19; Length 191; 99.1%; Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.5e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                 Ralston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 191 BP; 39 A; 47 C; 56 G; 49 T; 0 other;
                                                                                                                                                                                                                                                 Munger W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human growth hormone 3' UTR sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 23; 77pp; English
                                                                                                                                                                                                                                                 Bruno M, Muller S, Mumper R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ40410 standard; DNA; 191
                                                                                                              98WO-US02221.
                                                                                                                                                                     97US-0039709
                                                                                                                                                   98US-0012366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.1
Matches 107; Conservative
                                                                                                                                                                                                             (GENE-) GENEMEDICINE INC
                                                                                                                                                                                                                                                                                    WPI; 1998-467159/40
                                      WO9834952-A2
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                                                                                                              09-FEB-1998;
                                                                                                                                                                       LO-FEB-1997;
                                                                                                                                                     23-JAN-1998;
                                                                          13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ40410;
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AC AAZ40
XX AZX
DT 15-F
XX BH HMRI
XW WIld
KW WILD
XW CADC
δ
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This sequence represents the 3' unt4ranslated region from a human growth hormone gene. The invention relates to a novel plasmid comprising a cytomegaLovirus (CMY) promoter transcriptionally linked with an interferon alpha (IFN-alpha) coding sequence, and a growth hormone 3'-untranslated region (UTR). The plasmids can be used for treating a mammalian condition or disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human growth hormone 3'UTR; anti-angiogenic agent; expression plasmid; cancer; gene expression; mRNA stability; transfection; tumour activity; cytostatic; gene therapy; lung metastatic tumour; ss.
                                                                                                                                                                                            plasmids containing an interferon-alpha coding sequence, used for treatment of a mammalian condition or disease, particularly cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                              Length 191;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.3%; Score 96; DB 20; Length 19
Best Local Similarity 99.1%; Pred. No. 4.5e-21;
Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATATAT 227
                                                                                                                                                                                                                                                                                                                                                           Sequence 191 BP; 39 A; 47 C; 56 G; 49 T; 0 other;
                                                                                                                                               Rolland A, Ralston
                                                                                                                                                                                                                                               Disclosure; Page 27; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ50393 standard; DNA; 191 BP
                                                                     99WO-US05394.
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                                                                                               98US-0078654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human growth hormone 3'UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                               Nordstrom J, Pericle F,
                                                                                                                      (GENE-) GENEMEDICINE INC
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81..86
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999;
Homo sapiens
                       WO9947678-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000
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                                                                       L2-MAR-1999;
                                                                                               19-MAR-1998;
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                                                23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ50393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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AAX15886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; immunomodulatory; antisclerotic; demachogical; immunosuppressive; antisflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; antialzahemers; antiparkinsonian; antimicrobial; vulnerary; gene therapy; immune disorder; hyperproliferative; cardiovascular; angiogenic; neurological; infection; ss.
                                                                                                                                                                                                         -anglogenic agent. This was used in the construction of expression plasmid incorporating an anti-anglogenic agent for the treatment of mammalian diseases, especially cancer. This 3'UTR influences gene expression by controlling the accuracy and efficiency of RNA processing, manA stability and translation. The plasmids can be used for (in vivo) transfection of a cell in situ in order to modulate tumour activity. Anti-anglogenic gene inhibits growth of solid tumour and lung metastatic
                                                                                              Plasmids comprising tissue specific transcription elements linked to an anti-angiogenic gene is useful transfection of cells and treatment of,
                                                                                                                                                                    The present sequence is the 3'UTR of human growth hormone along with 3'flanking sequence. This sequence can be linked immediately following natural translation termination codon for a nucleotide encoding anti
                                                                                                                                                                                                                                                                                                                                                                                                        121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               27 agtgcctctcctggccctggaagttgccactccagtgcccaccagccttgtcctaataaa 86
                                                                                                                                                                                                                                                                                                                                                                                                                     42.3%; Score 96; DB 21; Length 191; 99.1%; Pred. No. 4.5e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATATTAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shi Y, Young PE, Ebner R, Soppet DR, Ruben SM;
                                                                                                                                                                                                                                                                                            tumours by intravenous or intramuscular delivery.
                                                                                                                                                                                                                                                                                                                   Sequence 191 BP; 39 A; 47 C; 56 G; 49 T; 0 other;
                                                Ralston R,
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                               Disclosure; Page 28; 103pp; English.
                                                Mehrens D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein cDNA #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF76860 standard; cDNA; 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-2000; 2000WO-US22350
98US-0094375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.1 Matches 107; Conservative
                         (VALE-) VALENTIS INC
                                                Szymanski P,
                                                                        WPI; 2000-183133/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200112776-A2
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-1999;
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                                                                                                                         e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF76860;
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                Min W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
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The present sequence is one of 18 nucleic acid molecules encoding novel human secreted proteins. The nucleic acids and proteins may be used in the prevention, diagnosis and treatment of diseases including immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher; sdiseases), cardiovascular diseases.

C. e.g. Scimitar syndrome, chaga's cardiomyopathy and coronary arteriosclerosis), anglogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may also be used as DNA similar nucleic assays to detect, and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may also be used as antigens in the production of antibodies and in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; growth hormone releasing hormone; GHRH; osteoporosis; cachexia; growth disorder; burn; sepsis; trauma; atherogenic; cardiovascular; chronic obstructive pulmonary disease; atherosclerotic; cerebrovascular; peripheral vascular disease; haemophilia; muscular atrophy; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCACCACCGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 18 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy ^{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NotI/Sall psk-GHRH plasmid fragment containing GHRH DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulators of protein expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 563 BP; 127 A; 139 C; 176 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.3%; Score 96; DB 22;
llarity 99.1%; Pred. No. 6.8e-21;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                    Claim 1; Page 358; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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2001-244245/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
107; Conserv
                                P-PSDB; AAB70079
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Matches
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Schwartz RJ;
Li X,
Eastman EM,
Draghia-Akli R,
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WPI; 1999-142950/12.

New vector for controlled expression of growth hormone releasing hormone - useful for treating osteoporosis and cachexia in humans, and to increase growth and improve the immune system of animals

Disclosure; Fig 6; 121pp; English.

hormone releasing hormone (GHRH). It is used in the construction of the vectors of the invention. The specification describes vectors comprising a cassette containing at east one sequence required for expression of GHRH, including a promoter, a linker that connects the 5' flanking sequence to a nucleic acid and includes a position for insertion of GHRH DNA but lacks the coding sequence of a gene naturally associated with it, 3'-flanking region, including untranslated and/or non-coding sequences, placed 3' to the position for insertion of GHRH DNA, and comprising a 3'-untranslated region (UTR). The vectors are used to deliver and express the human GHRH gene to a cell (Specifically human), in vivo or ex vivo, especially for treatment of osteoporosis, cachexia or growth disorders, but also burns, sepsis, trauma, chronic obstructive pulmonary disease, atheroselerctic, atherogenic, cardiovascular, cerebrovascular or peripheral vascular diseases, haemophilia, muscular atrophy (especially where associated with aging), muscular dystrophy etc. The present sequence contains the DNA sequence encoding human growth 

Sequence 1441 BP; 258 A; 474 C; 407 G; 302 T; 0 other;

1; Gaps Score 96; DB 20; Length 1441; Pred. No. 9.7e-21; 0; Mismatches 0; Indels 1 Query Match 42.3%; Best Local Similarity 99.1%; Matches 107; Conservative

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121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180 

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δλ QQ

181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATTAT 227

Search completed: January 17, 2002, 12:02:18 Job time: 17725 sec

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RELEVANT RESIDUES IN SEQ ID NO: PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Sweetser, et al.
JOURNAL: Genes & Dev.
  PAGES: 1318-1332
DATE: 1988
113.77
113.77
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113.77
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    (without alignments)
232.269 Million cell updates/sec
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                                                                                                                                                ; Search time 221.34 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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Sequence 1
Sequence (
                                                                                                                                                                                                                                                                         1 GCCTTAAGGGCCATATGGTG.......GGTGTCCTCTATAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-563-869A-1
US-08-563-869A-1
US-08-784-582-70
US-08-784-582-72
US-08-784-582-72
US-08-784-33-72
US-09-173-043-10
                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                              January 17, 2002, 07:04:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
                                                                                                                                                                                                                         US-09-242-202A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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93.4
93.4
72
60.6
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                                                                                                         OM nucleic
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                                                                                                                                              Run on:
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APPLI
                                                                                                    Sequence 1, 2 sequence 2, 2 sequence 4, 2 sequence 1, 2 sequence 1, 3 sequence 1, 3 sequence 3, 3 sequence 3, 4 sequence 4, 4 sequence 4, 5 sequence 4, 5 sequence 6, 6 se
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           Sequence
                                                                Sequence
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ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUUT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/273,411
                                         US-08-990-442-1
US-08-990-442-1
US-08-760-615-7
US-08-910-647-2
US-08-910-647-4
US-08-918-913-1
US-08-918-913-1
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US-08-918-913-1
US-08-918-913-3
US-08-918-913-3
US-08-63-998-3
US-08-63-998-3
US-08-63-998-3
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US-08-63-998-3
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ATTORNEY, AGENT INFORMATION:
NAME: Pabst, Patrea.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WULOOF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6558
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2771 base pairs
TYPE: nucleic acid
STANDEDNESS: double
TOPPLOGY: linear
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5: FROM 561 TO 629

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121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
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US-09-012-366-4
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APPLICANT: Robert
           ; TOPOLOGY:
US-08-321-686B-1
                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-012-366-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: King, Donna
APPLICANT: King, Donna
APPLICANT: Schneider, Gary B.
TITLE OF INVENTION: Treatment of
TITLE OF INVENTION: Osteopenias and No. 6153427-Human Transgenic
TITLE OF INVENTION: Transgenes
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wallenstein & Wagner, Ltd.
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                 Query Match 46.4%; Score 105.4; DB 1; Length 2771; Best Local Similarity 99.1%; Pred. No. 5.4e-24; Matches 106; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATAT 227
                                                                                               5: FROM 620 TO 2771
                                                                                                                                                                                                                              5: FROM 1 TO 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
MEDIUM TYPE: 800 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: WordPerfect 5.1
SOFTWARE: Simple Text ASCII (IBM format)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wallenstein & Wagner, Ltd.
STREET: 311 South Wacker Drive
STREET: 53rd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: not
PRIOR APPLICATION DATA: applicable
ATTORNEY/AGRYT INFORMATION:
NAME: BAITY, Alan L.
REGISTRATION NUMBER: 30,819
REFERENCE/DOCKET NUMBER: 1017P021
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/321,686B
FILING DATE: October 12, 1994
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                                                                                               NO:
                                                                                                                                                                                                                          ; RELEVANT RESIDUES IN SEQ ID NO: US-08-273-411-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08321686B
; Patent No. 6153427
                                                                                           RELEVANT RESIDUES IN SEQ ID
                                                                                                                                 Sweetser, et al.
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312)554-3300
TELEPAX: (312)554-3301
INFOTENTIAL (312)554-3301
SEQUENCE CHARACTERISTICS:
 Seeburg, et al
DNA
                                                                                                               PUBLICATION INFORMATION:
AUTHORS: Sweetser, et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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1986
                                                      239-249
1982
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4456 bp
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AUTHORS:
JOURNAL:
                                                                                                                                                  JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-321-686B-1
                                       VOLUME:
                                                                                                                                                                      VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                      PAGES:
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                                                                                                     121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
        DB 3; Length 4456;
                                                                                                                                                                                    Length 191;
                                               Indels
                                                                                                                                                               181 ATTAAGTIGCATCATTTTGTCTGACTAGGTGTCCTCTATAATTAT 227
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SUSAND MULLER
APPLICANT: Russ Mumper
APPLICANT: William Munger
APPLICANT: Walliam Munger
APPLICANT: Maria Bruno
TITLE OF INVENTION: IL-2 GENE EXPRESSION AND
TITLE OF INVENTION: DELIVERY SYSTEMS AND USES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
    Score 105.4; DB 3;
Pred. No. 6.4e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ore 96; DB 3; Le
ed. No. 1.8e-21;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: CALLLULIAGE
COMPUTER TRADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TARGET TO BATC.
CURRENT APPLICATION DATA:
APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/093/709
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: February 10, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09012366
Patent No. 6034072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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TELECOMMUNICATION INFORMATION:
      46.48;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.1%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkman, Charles S
                                                                                                                                                                                                                                                                                                                                                                Robert Ralston
Query Match
Best Local Similarity 99.1:
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 191 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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STATE: California
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1559 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCACCTTGTCCTAATAAA 1618
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             APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: No. 6110707mington, Karl D.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Quadde, Christian
APPLICANT: Guade, Christian
APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
WINNER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96; DB 3; Length 2086;
Pred. No. 4.4e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1619 ATTAAGTTGCATCATTTGTCTGACTAGGTGTCCTTCTATAATATAT 1666
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: CONCURTENTLY Herewith
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION WHERE: US 60/028,427
FILING DATE: 15-OCT-1996
PRIOR APPLICATION NUMBER: US 60/589,028
FILING DATE: 19-JAN-1996
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe A. APPLICANT: No. 6194176mington, Karl D. APPLICANT: Clark, Samuel A. APPLICANT: Thigpen, Anice E. APPLICANT: Quaade, Christian
                                                                                                                                                                                                                                                                Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UTSD: 514
    Newgard, Christopher B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08785271 Patent No. 6194176 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.38
Best Local Similarity 99.18
Matches 107; Conservative
                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, Whi
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                  Texas
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Gaps
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                                                                                                                                                                                                                                                                       APPLICANT: Newgard, Christopher B.
APPLICANT: Habban, Philippe
APPLICANT: Habban, Philippe
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Kruse, Fred
TITLE OF INVENTION: Recombinant Expression of Proteins From NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2086;
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Pred. No. 4.4e-21;
0; Mismatches 0; Indels
                                                                                      181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATATTAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,028
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRAINON NUMBER: 47, 642

REFERENCE/DOOKET NUMBER: UTSD:426\HYL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEPHONE: (512) 414-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
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                                                                                                                                                                                                                 Sequence 9, Application US/08589028
Patent No. 6087129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.3%;
Best Local Similarity 99.1%;
Matches 107; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-589-028-9
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CO
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US-08-589-028-9
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STATE: PA
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FEATURE:
                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-973-334-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-563-869A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
APPLICANT: Kruse, Fred
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
COMPRER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Gao, Guang-Ping
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
TITLE OF INVENTION: Methods of Production and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 No. 6261551ristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 96; DB 4; Lengtn 2002
Pred. No. 4.4e-21;
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                                                                                                                                                                              COUNTRY

ZIP: 77220

COMPUTER: FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,271
TITING DATE: CONCURRENTLY HEFEWITH
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                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-7AN-1996
ATOMES/AGENT INFORMATION:
NAME: Highlander, Stewen L.
REGISTRATION NUMBER: 37,642
REFERNCE/DOCKET NUMBER: UTSD:513
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
SEQUENCE CHARACTERISTICS:
LENGTH: 2086 base pairs
                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08973334
; Patent No. 6261551
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Box 40/, CITY: Spring House
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                                                                                                                                                                    Texas
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2501 AGTGCCTCTCCTGGCCCTGGAAGTTGGCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 2560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Associated Virus, Cell Lines, and
Methods of Production and Use
Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ATTAAGITGCATCATTTGTCTGACTAGGTGTCC-TCTATAATATTAT 227
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TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Box 457, 321 No. 6270996ristown Road
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0 Version 1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.4; DB 4;
Pred. No. 3.6e-20;
0; Mismatches 2;
                                                               SOFTWARE: PatentIn Release 1.0 Version 1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,334
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GNVPN012CIPUSA TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 540-9206 TELEFAX: (215) 540-5818 INFORMATION FOR SEQ ID NO: 1: SEGUENCE CHARACTERISTICS:
                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,014
FILING DATE: 05-UNN-1995
PRIOR APPLICATION NUMBER: US 08/549,489
FILING DATE: 27-COT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09563869A Patent No. 6270996 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wilson, James M. Fisher, Krishna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA ZIP: 19477
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                        NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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Best Local Similarity 97.2%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3653 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3653 base I
TYPE: nucleic acid
STRANDEDNESS: doubl
                  COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
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2501 AGTGCCTCTCCTGGCCCTGGAAGTTGGCACTCCAGTGCCCACCACCAGCATTGTCCTAATAAA 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATATTAT 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,674E
FILING DATE: July 3, 1997
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL THOOMATION:
GENERAL THOOMATION:
GENERAL SAID AND THE LIBERTY AND PROTICE OF INVENTION: RIBOZYME GENE LIBERRY AND PROTICE OF INVENTION: CESS FOR PREPARATION NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gabriel P. Katona
STREET: 230 Park Avenue, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.1%; Score 93.4; DB 4;
Best Local Similarity 97.2%; Pred. No. 3.6e-20;
Matches 105; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                            GNVPN013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08887674E Patent No. 6130092
                  REFERENCE/DOCKET NUMBER: GNVF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3653 base pairs
     REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1521..2405
US-08-549-489-1
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Matches 72; Conserv
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STATE:
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APPLICANT: Wilson, James M.
APPLICANT: Wilson, James M.
APPLICANT: Gao, Guang-Pling
TITLE OF INVENTION: No. 6281010el Adenovirus Gene Therapy Vehicle
TITLE OF INVENTION: and Cell Line
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 No. 6281010ristown Road
CITT: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.1%; Score 93.4; DB 4; Length 3653; Best Local Similarity 97.2%; Pred. No. 3.6e-20; Matches 105; Conservative 0; Mismatches 2; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ATTAAGTTGCATCATTTTGTCTGACTAGGTGTCC-TCTATAATATTAT 227
                                                                                 APPLICATION NUMBER: 08/973,334
APPLICATION NUMBER: 08/973,334
FILING DATE: COURNOWN
APPLICATION NUMBER: US 08/549,489
FILING DATE: 27-0CT-1995
ATORNEY/AGET INFORMATION:
NAME: BAK, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNYPNO12CIPUSA
TELECHMUNICATION INFORMATION:
TELECHMONE: (215) 540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIE: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/563,869A
FILING DATE: 03-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1521..2405
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3653 base pairs
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; Patent No. 6281010
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
FEATURE:
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Indels

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Length 792;

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APPLICANT: MCGATY, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARTS STATEM: TO LOSS/MS DOS SOFTWARTS PAGE 1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582 FILING DATE: CONCURTENTLY Herewith CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 60/028,427 FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427 APPLICATION NUMBER: US 60/028,427 APPLICATION NUMBER: US 60/028,427 APPLICATION NUMBER: US 08/589,028 FILING DATE: 19-JAN-1996 ATTORNEY/AGRNT INFORMATION:
                                                                                  Meyard, Christopher B.
Halban, Philippe A.
No. 6110707mington, Karl D.
                                                                                                                                                                                                                                                                                                                                                     Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 Sequence 72, Application US/08784582 Patent No. 6110707 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             Thigpen, Anice E.
Quaade, Christian
Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 2356 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.73
Best Local Similarity 84.2
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                 Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.
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                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                 APPLICANT: Newgard, Christopher B.
APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: No. 6110707minqton, Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice B.
APPLICANT: Quade, Christian
APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.6; DB 3; Length 1884;
Pred. No. 5.9e-10;
0; Mismatches 14; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Concurrently Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/784,582
FILING DATE: Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                Sequence 70, Application US/08784582
Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 70:
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Best Local Similarity 84.2%;
Matches 80; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                      781 ATTAAGTTGCAT 792
181 ATTAAGTTGCAT 192
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                                                                                                        RESULT 11
US-08-784-582-70
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US-08-784-582-70
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                                                                              18 GIGAGIGGAICCCITGACCCCAGGCGGGGAI-GGGGAGACCIGIAGICAGAGCCCCCGGG 76
                                            1;
Length 2356;
                                          14; Indels
26.7%; Score 60.6; DB 3;
84.2%; Pred. No. 6.4e-10;
tive 0; Mismatches 14;
                                                                                                                                                               77 CAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGA 111
                                                                                                                                                                                                     878 cagcacagecaargcccgrccrrgcccrgcagaa 912
                                                                                                                                                                                                                                                                                 US-08-068-754-3/c
Sequence 3, Application US/08068754
Patent No. 6023011
GENERAL INFORMATION:
APPLICANT: Vale, Wyle W.
APPLICANT: Stenzel-Poore, Mary P.
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RESULT

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APPLICATION NUMBER: US/09/325,926
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Madison
STATE: New Jersey
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ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 42;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stenzel-Poore, Mary P.
Koob, George F.
Heinrichs, Stephen C.
TITLE OF INVENTION: CORTICOTROPIN-RELEASING FACTOR
OVERPRODUCING TRANSGENIC MICE
                                                                                                                         ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                      TITLE OF INVENTION: CORTICOTROPIN-RELEASING FACTOR TITLE OF INVENTION: OVERPRODUCING TRANSGENIC MICE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 CCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAA 176
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,754
FILING DATE: 28 WAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 CCCTGGAAGTTGCCACTCCAGTGCCCACCACCTTGTCCTAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Oligonucleotide
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09325926
Patent No. 6166287
GENERAL INFORMATION:
APPLICANT: Vale, Wyle W.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
ATORNEY/AGENT INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/POCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEFRAX: 619-546-939
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
APPLICANT: Koob, George F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: CA
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TYPE: nucleic acid
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                                                                                                         CORRESPONDENCE ADDRESS:
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US-09-325-926-3/c
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GENERAL INFORMATION:
APPLICANT: de Vries, Jan
APPLICANT: Jeah, Chung-Her
APPLICANT: Narula, Satwant
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screens
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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100.0%; Pred. No. 0.0001;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,754
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P41 9397
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: Oligonucleotide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,162
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: US07/869914
FILING DATE: 16-APR-1992
APPLICATION NUMBER: US07/770081
FILING DATE: 03-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,024
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: JB0214
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Best Local Similarity 100.0%; Pr
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STRANDEDNESS: single
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| TELEPHONE: 201 822 7375 | TELEFAX: 201 822 7039 | TELEFAX: 219165 | TELEFX: 219165 | SEQUENCE CHARACTERISTICS: ENGTH: 51 base pairs | TYPE: nucleic acid | STRANDEDNESS: single | TOPOLOGY: Linear | TOPO
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0; Gaps Query Match 18.5%; Score 42; DB 2; Length 51; Best Local Similarity 100.0%; Pred. No. 0.00011; Matches 42; Conservative 0; Mismatches 0; Indels δŏ qq

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Search completed: January 17, 2002, 11:52:06 Job time: 17253 sec

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January 17, 2002, 11:48:13 ; Search time 10436.3 Seconds (without alignments) 17.388 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                          1472140 segs, 8248589755 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1 GCCTTAAGGGC 11
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Sequenc Sequenc Sequenc Sequenc Sequenc	Sequenc Sequenc Sequenc Sequenc	AR075083 Sequence AR075083 Sequence AR076083 Sequence AR076089 Sequence AR075075 Sequence AX088904 Sequence AX088908 Sequence	Sequence Sequence Sequence dicago sa Sequence Sequence Sequence	uman ST BN1-25 Unident Unident Unident Unident Unident Sequenc Sequenc Uman ST H.sapi	AJ290153 Homo sapi AJ290145 Homo sapi K03275 D.melanogas X95449 Endogenous X95450 Endogenous X10908 D. melanoga Z66533 Endogenous	PAT 17-MAR-2001	stridium group; lllus. sterase activity and nucleic l; l;
ID	AX088916 AR069952 AX088922 AR069934 AR076077	AR069933 AR076076 AR075081 AR069956 AR076090	AR069950 AR075083 AR069955 AR076089 AR075075 AR076086	AR075077 AR076085 AX088906 MSZ99636 AX088919 AX088920 AX088921 G05653		HSA290153 HSA290145 DROTN882 ESRVLTRL5 ESRVLTRL6 ENJRVLTR3 ALIGNMENTS	DNA nt WO0114534. 75	Bacillus/Clos us group; Baci ,K.M. ectin acetyles 17 01-MAR-2001 c. (US) lifiers acillus subtil
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Length	17 17 33 33 34 34	36 36 40 40	44444000 CCCC88447	58 58 184 185 185 243	268 2771 2775 2775 2775 2775 4700 4700 4700	4 4 4 4 4 4 20000004 40000000	17 from [7] GI:13 subtilis	Bacteria, Firmicutes, Bacillus/Staphylococcu E 1 (bases 1 to 17) S Thomas, M.D. and Brown, Polypeptides having peacids encoding same acids encoding same L Patent: WO 0114534-A 1 Novozymes Biotech, Inc Location/Qual rce 1 17
ch					000000000000		16 1 16 1 16 1 16 1 16 1 16 1 16 1 16	la; 18/8 368 368 M.D.M.D.D. Ti WG
Query Match	1000	2001			100000000000000000000000000000000000000	0000000	8893 8893 8893 111	ter illi (bas (bas yper ds ds ent
Score			1222222	17777777		######################################	AX088916 AX088916 AX088916 AX088916	Bac Bac 1 Thor Poly Pati Nov
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BASE COUNT ORIGIN

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1 (bases 1 to 34)
Sloma, A., Sternberg, D., Adams, L.F. and Brown, S.
Methods for producing polypeptides in mutants of bacillus cells
Patent: US 5958728 - 19 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                            18-FEB-2000
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Sequence 19 from patent US 5891701.
AR069934
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Sequence 18 from patent US 5891701.
AR069933
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Best Local Similarity 100.
Matches 11; Conservative
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                 2 GCCTTAAGGGC 12
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     1 GCCTTAAGGGC 11
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Matches 11; Conserv
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AR069933/C
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SOURCE
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FEATURES
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Bacillus subtilis
Bacillus subtilis
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 33)
Thomas, M. D. and Brown, K.M.
Polypeptides having pectin acetylesterase activity and nucleic acids encoding same
Patent: WO 0114534-A 23 01-MAR-2001;
Novozymes Biotech, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
1 (bases 1 to 33)
1 (bases 1 to 33)
Sloma, A. and Christianson, L.
Nucleic acids encoding a polypeptide having protease activity
Patent: US 5891701-A 39 06-APR-1999;
Location/Qualifiers
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                                                                       Length 17;
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100.0%; Score 11; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels
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ive 0; Mismatches 0;
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/organism="Bacillus subtilis"
/db_xref="taxon:1423"
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Sequence 23 from Patent W00114534.
AX088922
/db_xref="taxon:1423"
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9
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Sequence 39 from patent
AR069952
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Best Local Similarity 100.
Matches 11, Conservative
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Matches 11; Conserv
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BASE COUNT

ORIGIN

DEFINITION

RESULT AX088922 LOCUS

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ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL FEATURES BASE COUNT

JOURNAL FEATURES

AUTHORS TITLE

REFERENCE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT AR069952

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us-09-242-202a-10\_copy\_l\_ll.rge

ORGANISM

REFERENCE AUTHORS source

JOURNAL

TITLE

FEATURES

BASE COUNT ORIGIN

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1 (bases 1 to 40)
Sloma,A., Sternberg,D., Adams,L.F. and Brown,S.
Methods for producing polypeptides in mutants of bacillus cells
Patent: US 5958728 A. 32 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   1 (bases 1 to 40)
Sloma,A. and Christianson,L.
Nucleic acids encoding polypeptide having protease activity
Patent: US 5891701-A 46 06-APR-1999;
Location/Qualifiers
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ch 100.0%; Score 11; DB 6; Length 37; 1. Similarity 100.0%; Pred. No. 1.1e+04; 11; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0;
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Sequence 37 from patent US 5891701.
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14 c 13 g
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Unclassified.
1 (bases 1 to 36)
Sloma,A., Sternberg,D., Adams,L.F. and Brown,S.
Methods for producing polypeptides in mutants of bacillus cells Patent: US 5958728-A 18 28-SEP-1999;
Location/Qualifiers
                              1 (bases 1 to 36)
Sloma, A. and Christianson, L.
Nucleic acids encoding a polypeptide having protease activity
Patent: Uccation/Qualifiers
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Widner,W., Sloma,A. and Thomas,M.D.
Methods for producing a polypeptide in a bacillus cell
Patent: US 5955310.A 7 21-SEP-1999;
Location/Qualifiers
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Sequence 18 from patent US 5958728.
AR076076 : GI:10002822
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Sequence 7 from patent US 5955310.
AR075081.1 GI:10001833
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Sloma, A., Sternberg, D., Adams, L.F. and Brown, S.
Methods for producing polypeptides in mutants of bacillus cells
Patent: US 5958728 A 25 28-SEP-1999;
Location/Qualifiers
                                                    Unclassified.

1 (bases 1 to 42)
1 (bases 1 to 42)
Sloma.A. and Christianson,L.
Nucleic acids encoding a polypeptide having protease activity
Patent: US 5891701-A 37 06-APR-1999;
Location/Qualifiers
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Widner,W., Sloma,A. and Thomas,M.D.
Methods for producing a polypeptide in a bacillus cell
Patent: US 5955310-A 9 21-SEP-1999;
Location/Qualifiers
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Sequence 9 from patent US 5955310.
AR075083.1 GI:10001835
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Sequence 25 from patent US 5958728.
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Sloma, A., Sternberg, D., Adams, L.F. and Brown, S.
Methods for producing polypeptides in mutants of bacillus cells
Patent: US 5958728 A 31 28-SEP-1999;
Location/Qualifiers
                                         Gaps
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Slowa, A. and Christlanson, L.
Nucleic acids encoding a polypeptide having protease activity
Patent: US 5891701-A 45 06-APR-1999;
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0;
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Sequence 31 from patent US 5958728.
AR076089.1 GI:10002835
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Sequence 45 from patent US 5891701.
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PCR primer 18 used Bacillus subtilis

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AAV82401
AAV38594
AAV82400
AAZ23328
AAD09904
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AAF62646
AAF62647
AAV21719
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AAA32016
AAA31512
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AAD09901
AAF62632
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AAX34334
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AAD09922
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AAD09924
AAD09931
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AAZ23330
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AAZ23323
AAZ23324
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AAV21720
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       AAV21736 standard; cDNA; 11
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     Nelson PJ;
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     14-AUG-1997;
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Bacillus amyloliqu
Bacillus amyloliqu
Bacillus amyL prom
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PCR primer #1 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Short consensus am
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PCR primer 19 used
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                                                                                                                                                                          ; Search time 599.86 Seconds
(without alignments)
15.721 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                US-09-242-202A-10_COPY_1_11
                                                                                                                                                                             January 17, 2002, 12:02:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAD09925
AAD09928
AAF62648
AAV38595
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AAZ23342
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AAF62642
AAZ23344
AAZ23348
                                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapovt 1.0
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Maximum DB seq length: 200000000
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Match
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Score

Result No.

10 10 10 10

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comprise a human derived promoter or mammalian homologue and sequence acceptance site that is designed to directionally accept sequence specific products from RT-PCR based cloning strategies via a unique site within an interrupted palindrome recognition sequence for a restriction endonuclease which is incorporated into the PCR ptimer. In this embodiment, the palindrome recognition requence is for Bgll. The 5' acceptance site is given in AAV21735. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences, and emmune responses to the target sequences with little or no immune response to the other vector components.
polynucleotide vectors such as pITL (see AAV21724).
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 other;
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Gaps
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0
               100.0%; Score 11; DB 19; Length 11; 100.0%; Pred. No. 38+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.00
Thes 11; Conservative
                                                                    1 GCCTTAAGGGC 11
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1 gccttaagggc 11 Dp

AAZ23342 standard; DNA; 17 BP. AAZ23342; AAZ23342 RESULT 

06-DEC-1999 (first entry)

Bacillus amyloliquefaciens consensus amyQ gene promoter PCR primer 2.

Tandem promoter; consensus promoter; enzyme production; hormone; antibody; reporter; marker gene; cell regulation; PCR primer; amyQ; alpha-amylase; ss.

Synthetic

Bacillus amyloliquefaciens.

W09943835-A2

02-SEP-1999.

99WO-US04360 26-FEB-1999; 26-FEB-1998;

Example 18; Column 25; 54pp; English.

98US-0031442

(NOVO ) NOVO NORDISK BIOTECH INC.

Widner W, Sloma A, Thomas MD;

WPI; 1999-561370/47.

This invention describes a novel method for the production of a Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes Example 18; Page 35; 90pp; English.

polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine protease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a PCR primer used to amplify the Bacillus amyloliquefaciens consensus amyQ promoter.

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Gaps
                                                                                                                                                                                                                      Bacillus cell; tandem promoter; consensus promoter; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryllIA promoter; subtilisin Carlsberg gene promoter; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters
                                                        ·,
                                                                                                                                                                                                    PCR primer #1 for constructing mutated consensus amyQ promoter
                                     Length 17;
                                                        Indels
                                     DB 20;
3.2e+02;
        Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;
                                                        0; Mismatches
                                    Score 11;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                              Thomas MD;
                                    100.0%;
100.0%;
                                                                                                                                            AAD09919 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                          (NOVO-) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                                     99US-0258377.
                                                                                                                                                                                                                                                                                                                                        98US-0031442.
                                                                                                                                                                                                                                                             Bacillus amyloliquefaciens
                                                                                                                                                                                  (first entry)
                                  Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Sloma A,
                                                                           1 GCCTTAAGGGC 11
                                                                                            2 gccttaagggc 12
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                                                                                                                                                                                                                                                                               US6255076-B1.
                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
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                                                                                                                                                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                              Widner W,
                                                                                                                                                               AAD09919;
                                                                                                                                   AAD09919
                                                                                                                          RESULT
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The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Bach promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem promoter comprises amyt promoter, amyQ promoter, apry promoter, crylIIA promoter, amyQ promoter, apry promoter, crylIIA promoter, cultivation consensus promoters of the amyL promoter, amyQ promoter, apry promoter, crylIIA promoter or subtilisin Carlsberg gene promoter have the sequence TTGACA for the -35 region and TATAAT for the -10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain. The present sequence is a PCR primer used in the construction of a consensus mutated Bacillus amyloliquefaciens alpha-amylase (amyQ) consensus mutated Bacillus amyloliquefaciens alpha-amylase (amyQ) stream region of the amyQ promoter, used in the exemplification of the invention.

Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;

Score 11; DB 22; Length 17; Pred. No. 3.2e+02; 100.0%; Query Match Best Local Similarity

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alpha-amylase; SAVINASE; ss.
                                             W09943835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09943835-A2
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                                                                                 26-FEB-1999;
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                                                              02-SEP-1999
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                  Synthetic.
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                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptide having pectin acetylesterase activity useful for degrading pectic substances and in degradation or modification of acetylated pectins and plant cell walls .
                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to Bacillus subtilis pectin acetylesterase protein. The invention is useful for degrading a pectic substance. It is also useful for degrading soluble and insoluble pectins with varying degrees of esterification, clarification etc. The protein may be used alone or in combination with other enzymes for the degradation or modification of acetylated pectins, degradation or modification of plant cell walls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens short consensus amyQ promoter PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tandem promoter; consensus promoter; enzyme production; hormone;
antibody; reporter; marker gene; cell regulation; PCR primer; amyQ;
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0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                      Pectin acetylesterase; degrade; plant cell wall; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 11; DB 22;
100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;
Mismatches
                                                                                                                                                                                                                                                                                                                                                              Example 9; Column 28; 35pp; English.
                                                                                                                                      amyQ promoter oligonucleotide #3
                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK BIOTECH INC
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                                                                                AAF62642 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ23344 standard; DNA; 33
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                        Brown KM;
                                                                                                                                                                                                                                                                                                         WPI; 2001-190946/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCCTTAAGGGC 11
                            1 GCCTTAAGGGC 11
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Best Local Similarity
Matches 11; Conserv
                                                                                                                    03-MAY-2001
                                                                                                                                                                                                                                                   26-AUG-1999;
                                                                                                                                                                                            US6184028-B1
                                                                                                                                                                                                              06-FEB-2001
11;
                                                                                                                                                                                                                                                                                        Thomas MD,
                                                                                                                                                                         Synthetic.
                                                                                                  AAF62642;
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Matches
                                                                      AAZ23344
ID AAZ2
XX
AC AAZ2
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DT 06-D
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DE Baci
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KW Tand
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This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine protease, maltgenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters etc. The specified promoters provide increased expression of the sequence which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a PCR primer used to amplify the Bacillus amyloliquefaciens short consensus amyQ promoter which is gene expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tandem promoter; consensus promoter; enzyme production; hormone;
antibody; reporter; marker gene; cell regulation; PCR primer; amyQ;
alpha-amylase; SAVINASE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes
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Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 4 A; 11 C; 10 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 19; Page 36; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ23348 standard; DNA; 33 BP
                                                                                                                                                                                                                     99WO-US04360.
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Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus amyloliquefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Widner W, Sloma A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-561370/47.
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AAD09925
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                                                                                                                                                              This invention describes a novel method for the production of a polypeptide in Bacillus using specific tandem or consensus promoters. The method is used to produce homologous or particularly heterologous proteins, particularly enzymes (specifically serine protease, maltogenic alpha-amylase and pullulanase), but also hormones, antibodies, reporters alpha-amylase and pullulanase), but also hormones, antibodies, reporters which encodes the polypeptide of the invention. After incorporation of the nucleic acid construct of the invention, any marker gene may be deleted, resulting in a cell that is preferred for environmental and regulatory regions. This sequence represents a PCR primer used to amplify the Bacillus amyloliquefaciens short consensus amyQ trimer promoter. Which savannasE(RTM) gene expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease; detergent; surfactant; leather processing; debittering;
                                                                                                    Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                          Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flavour; PCR; primer; amyL; amylase; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 11; DB 20;
100.0%; Pred. No. 3.4e+02;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 Sequence 33 BP; 4 A; 11 C; 10 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus amyL promoter PCR primer term1Sfi.
                                                                                                                                        Example 25; Page 41; 90pp; English.
                        (NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO NORDISK BIOTECH INC.
                                                   Thomas MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV82419 standard; DNA; 33 BP.
 98US-0031442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US12005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus amyloliquefaciens.
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                  Sloma A,
                                                                          WPI; 1999-561370/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCCTTAAGGGC 11
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 26-FEB-1998;
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                                                  Widner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV82419
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AAV82419
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Example 12; Page 36; 77pp; English.

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The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conductve for the production of the polypeptide. Each promoter sequence of the tandem promoter is operably planked to a nucleic acid sequence encoding the polypeptide. The tandem promoter comprises anyl promoter, any promoter, aprh promoter, cryllin promoter or subtilisin Carisberg gene promoter. The consensus promoters or subtilisin Carisberg gene promoter. The consensus promoters or subtilisin Carisberg gene promoter aprh promoter Troack for the "35 region and TATAAT for the "10 region. The method further comprises isolating the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain.
Primers termISFi and 21Sfi (see AAV82419-20) were used for the PCR amplification of the promoter region of the TERMAMYL amylase amyl gene of Bacillus amyloliquefaciens. Primer termISFi was used to add an Sfil site to the 5' end of the promoter. The Bacillus APT/O procease gene (see AAV82382) in vector pSJ2882-MCS, useful in detergent compositions and in leather processing. Host cells, vectors and methods for recombinant production of the
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aprH promoter;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters -
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                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cell; tandem promoter; consensus promoter; polypeptide production; amyL promoter; amyQ promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Short consensus amyQ promoter amplifying PCR primer.
                                                                                                                                                                                                                                                                                     100.0%; Score 11; DB 20;
100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                          Sequence 33 BP; 4 A; 11 C; 9 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 19; Column 26; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD09925 standard; DNA; 33 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                             Matches 11; Conservative
                                                                                                                                                                                           protease are provided.
                                                                                                                                                                                                                                                                                                                                                                     1 GCCTTAAGGGC 11
                                                                                                                                                                                                                                                                                                                                                                                            5 gccttaagggc 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sloma A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-440518/47.
                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                         Query Match
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The present invention relates to a method for producing a polypeptide, comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters. The Bacillus is cultivated in a medium conducive for the production of the polypeptide. Each promoter sequence of the tandem promoter is operably linked to a nucleic acid sequence encoding the polypeptide. The tandem promoter comprises amyL promoter, amyQ promoter, aprH promoter, crylIIA promoter comptises amyL promoter, amyQ promoter, aprH promoter, crylIIA promoter, containing the promoter, crylIIA promoter, containing the promoter, aprH promoter, crylIIA promoter, containing the polypeptide from the cultivation medium. The method is useful for producing a polypeptide in a Bacillus strain.

The present sequence is a PCR primer used in the construction of a short consensus mutated Bacillus amyloliquefaciens alpha-amylase (amyQ) dimer promoter gene expression cassette, used in the exemplification of
                                                                                                                                                                               ö
The present sequence is a PCR primer used in the construction of a short consensus mutated Bacilius amyloliquefaciens alpha-amylase (amyQ) promoter gene expression cassette, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus cell; tandem promoter; consensus promoter; polypeptide production; amyL promoter; amyQ promoter; aprH promoter; cryIIIA promoter; subtilisin Carlsberg gene promoter; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing a polypeptide in a Bacillus strain comprises cultivating a Bacillus cell, which contains a nucleic acid construct comprising a tandem promoter and consensus promoters
                                                                                                                                                                               Gaps
                                                                                                                                                                               ;
0
                                                                                                                                            Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Short consensus amyQ dimer promoter amplifying PCR primer.
                                                                                                                                                                             Indels
                                                                                                                                                                               ;
                                                                                                                                          100.0%; Score 11; DB 22; 100.0%; Pred. No. 3.4e+02;
                                                                                    Sequence 33 BP; 4 A; 11 C; 10 G; 8 T; 0 other;
                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 25; Column 30; 54pp; English
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                                                                                                                                                                                                                                                                                                                                       AAD09928 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                               1 GCCTTAAGGGC 11
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                                                                                                                                                                                                                                                   2 gccttaagggc 12
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Sequence 33 BP; 4 A; 11 C; 10 G; 8 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide having pectin acetylesterase activity useful for degrading pectic substances and in degradation or modification of acetylated pectins and plant cell walls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bacillus subtilis pectin acetylesterase protein. The invention is useful for degrading a pectic substance. It is also useful for degrading soluble and insoluble pectins with varying degrees of esterification. Clarification etc. The protein may be used alone or in combination with other enzymes for the degradation or modification of acetylated pectins, degradation or modification of acetylated pectins, degradation or modification of plant cell walls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                              Gaps
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   Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer 19 used to amplify a portion of the amyE gene.
                             Indels
                                                                                                                                                                                                                                                                                Pectin acetylesterase; degrade; plant cell wall; ss.
Score 11; DB 22;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 11; DB 22;
100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33 BP; 4 A; 11 C; 10 G; 8 T; 0 other;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Column 29; 35pp; English
                                                                                                                                                                                                                                                   amyQ promoter oligonucleotide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO NORDISK BIOTECH INC
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0
                                                                                                                                                            AAF62648 standard; DNA; 33 BP
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100.0%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-190946/19.
                                                          11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 gccttaagggc 12
                                                                                    2 gccttaagggc 12
 Query Match
Best Local Similarity
Matches 11; Conserv
                                                          1 GCCTTAAGGGC
                                                                                                                                                                                                                                                                                                                                           US6184028-B1
                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999;
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                                                                                                                                                                                                                      03-MAY-2001
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                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                          AAF62648;
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                                                                                                                                  RESULT
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amplification of a downstream portion (nucleotides 445-953,
where the A of the ATG start codon is +1) of the alpha-amylase
where the A of the ATG start codon is +1) of the alpha-amylase
amyg gene from Bacillus subtilis A 164 chromosomal DNA. Primer 19
includes Sfil and NotI sites. An upstream portion of the amyg gene
(nucleotides -421 to +77) was amplified using primers 17 and 18
cese ANV82399-4400. The 2 fragments were then spliced by PCR using
primers 17 and 20. A splicing by overlap extension (SoB) reaction
was performed to create a deleted version of the amyg gene and
cells having a deleted spoilAC gene, a deleted amyg gene and
deleted protease genes have been constructed. These can be used in
the production of heterologous polypeptides. The invention also
relates to Bacillus proteases (see AAW89547-48) suitable for use in
                                                                                                                                                                                                                                           Primers 19 and 20 (see AAV82401-02) are designed for use in the PCR
                                                                                                                                               Novel protease from Bacillus subtilis \text{LC20} - useful in laundry and dishwashing detergents and for leather processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing polypeptides in Bacillus cells - which are modified to reduce production of surfactin, useful for, e.g. producing hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amyE gene; strain A164; mutant Bacillus; biosynthesis; surfactin;
production; hormone; enzyme; receptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer 18 used to amplify a portion of the amyE gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 11; DB 20; 100.0%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34 BP; 5 A; 10 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                         Example 5; Page 30; 77pp; English.
                                     (NOVO ) NOVO NORDISK BIOTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                        Christianson L, Sloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCCTTAAGGGC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 11; Conserv
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Bacillus subtilis.
 12-JUN-1997;
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18-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primers AAV38593-94 and AAV38595-96 were used to amplify the different portions of the amyE gene of Bacillus subtilis strain A164. The portions were cloned to create a partially deleted amyE gene. This was used in the course of the invention. The specification describes the production of a polypeptide. This comprises culturing a mutant Bacillus that includes nucleic acid encoding the polypeptide and nucleic acid containing a modified form of at least 1 gene involved in biosynthesis of a surfactin or its isoforms. The mutant organism produces less surfactin, or isoform, than wild type Bacillus. The method may be used heterologous or homologous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  - which are modified to
or, e.g. producing hormones
   strain A164; mutant Bacillus; biosynthesis; surfactin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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 amyE gene; strain A164; mutant Bacillus; biosynthesis,
production; hormone; enzyme; receptor; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-amylase; amyE gene; protease; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 11; DB 19; Similarity 100.0%; Pred. No. 3.4e+02; 11; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                          Producing polypeptides in Bacillus cells - wreduce production of surfactin, useful for, or enzymes
                                                                                                                                                                                                                                                                                                                           Sternberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 25; 43pp; English.
                                                                                                                                                                                                                                                                                  (NOVO ) NOVO NORDISK BIOTECH INC.
                                                                                                                                                                                                                                                                                                                         Sloma A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV82401 standard; DNA; 34 BP.
                                                                                                                                                                                            97WO-US21084
                                                                                                                                                                                                                             97US-0049441
                                                                                                                                                                                                                                               96US-0749521
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                                                                                                                                                                                                                                                                                                                       Brown S,
                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-312483/27
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                                                      Synthetic.
Bacillus subtilis.
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Bacillus subtilis.
                                                                                                             WO9822598-A1
                                                                                                                                                                                    18-NOV-1997;
                                                                                                                                                                                                                           12-JUN-1997;
                                                                                                                                                                                                                                               18-NOV-1996;
                                                                                                                                                   28-MAY-1998
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                                                                                                                                                                                                                                                                                                                     Adams LF,
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Query Match

Best Loca Matches

AAV82401;

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Gaps

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Length 34; Indels

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                                           PCR primers AAV38593-94 and AAV38595-96 were used to amplify the different portions of the amyE gene of Bacillus subtilis strain A164. The portions were cloned to create a partially deleted amyE gene. This was used in the course of the invention. The specification describes the production of a polypeptide. This comprises culturing a mutant Bacillus that includes nucleic acid encoding the polypeptide and nucleic acid containing a modified form of at least 1 gene involved in biosynthesis of a surfactin or its isoforms. The mutant organism produces less to produce hormones, enzymes and receptors, which are either heterologous or homologous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primers 17 and 18 (see AAV82399-400) are designed for use in the PCR amplification of an upstream portion (nucleotides -421 to +77, where the A of the ATG start codon is +1) of the alpha-amylase amyE gene from Bacillus subtilis A164 chromosomal DNA. Primer 18 includes Sfil and NoII sites. A downstream portion of the amyE gene (nucleotides 445-953) was amplified using primers 19 and 20 (see primers 17 and 20. A splicing by overlap extension (SOE) reaction was performed to create a deleted version of the amyE gene. Mutant host cells having a deleted spoilAC gene, a deleted amyE gene and deleted protease genes have been constructed. These can be used in
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protease from Bacillus subtilis LC20 – useful in laundry and dishwashing detergents and for leather processing
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                                                                                                                                                                                                                                   Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase; amyE gene; protease; PCR; primer; ss.
                                                                                                                                                                                                                                 Query Match 100.0%; Score 11; DB 19; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                Sequence 36 BP; 11 A; 12 C; 10 G; 3 T; 0 other;
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                     Example 5; Page 25; 43pp; English
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                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                     AAV82400 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Christianson L, Sloma A;
                                                                                                                                                                                                                                                                                  1 GCCTTAAGGGC 11
                                                                                                                                                                                                                                                                                                22 GCCTTAAGGGC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-1998;
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  or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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antibody; reporter; marker gene; cell regulation; serine protease;
                                                                                                                                                                                                                                                                                                       Gaps
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the production of heterologous polypeptides. The invention also relates to Bacillus proteases (see AAW89547-48) suitable for use in detergent compositions and in leather processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of polypeptide in Bacillus using specific promoters, particularly for producing enzymes \, \,^{\circ}
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                                                                                                                                                                                                                               Length 36;
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100.0%; Score 11; DB 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
                                                                                                                               Sequence 36 BP; 11 A; 12 C; 10 G; 3 T; 0 other;
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Best Local Similarity 100.0
Matches 11; Conservative
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SAVINASE; PCR primer; ss.
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Bacillus licheniformis.
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Search completed: January 17, 2002, 12:02:19 Job time: 17726 sec

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9. AV146659 HSC09H082 n

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AZ075637 RPCI-23-4
AA303217 EST14478
AA498912 v183d08.r
BE689384 RC2-UT002
FF18421 HSPD03004 H
AW197056 xb15f06.x
                                                                        BB143920 BB143920
AV321312 AV321312
F25526 HSPD12608 H
AW920467 EST35171
N23615 yv99f09.rl
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//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone_lib="Human fetal heart, Lambda ZAP Express"
//db_host="E. coli XLI-Blue"
//note="Vector: Lambda ZAP Express; Site_l: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10
                                                                                                                      BG552774 dab75902.
BI262529 ESTC5 Sub
BB152224 BB152224
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AV281033 AV281033
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
                                                                                                                                                                                                                    AV649344 AV649344
                                                                                                                                                                                                                                                                                                                                                                 AA093528 100 bp mRNA EST 25-OCT-1996
C10250.seq.F Human fetal heart, Lambda 2AP Express Homo sapiens
CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banting institute, 100 College St., Toronto, Ontario, M5GlL5 Tel: 4169788758
Fax: 4169785650
AI800916 v
BF605530 2
AZ075637 F
AA303217 F
                                                                                                                                                                                                                                                                                              BB390531 AZ217098
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Department of Laboratory Medicine and Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUCR PRIMERS
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                            AA303217
AA498912
BE698384
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AZ217098
                                                                                   AV321312
                                                                                                                                                                      AV146659
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                                                               AW197056
                                                                          BB143920
                                                                                                     AW920467
                                                                                                                       BG552774
                                                                                                                                                                                       AA094468
                                                                                                                                                                                                AU127469
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cDNAs from fetal heart (1996)
Unpublished (1996)
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                                                                                                                N2361
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TITLE
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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AA093528
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SOURCE
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AQ012949 CIT-HSP-2
AW308236 3366 MARC
AI303597 u181a12.x
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AQ355689 CITBI-E1-
AA345723 EST51785
AZ123745 RPCI-23-4
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AZ119770 RPCI-23-4
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BE245846 TCBAP1E19
                                                               ; Search time 6501.33 Seconds (without alignments) 18.181 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                      22703874
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                    11351937 segs, 5372889281 residues
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                               January 17, 2002, 08:54:00
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Maximum Match 100%
Listing first 45 summaries
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A2123745
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Gapop 10.0 , Gapext 1.0
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Searched:

us-09-242-202a-10\_copy\_1\_11.rst

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                                       Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                114 GCCTTAAGGGC 104
                                                                         1 GCCTTAAGGGC 11
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                   Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                          AZ119770 115 bp DNA GSS 12-MAY-2000 RPCI-23-479A23.TV RPCI-23 Mus musculus genomic clone RPCI-23-479A23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Jases 1 to 115)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
broats ite_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
32 c 28 g 20 t
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.bifalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.corg/tdb/bac_ends/mouse/bac_end_intro.html
weeks). cDNA was synthesized using a XhoI-Oligo dradaptor primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
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                                                                                                                                                            Length 100;
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Other_GSSs.RPCI-23-479A23.TJ
Contect: Shaying Zhoo
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                      Score 11; DB 10;
Pred. No. 7.5e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="RPCI-23-479A23"
/clone_lib="RPCI-23"
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100.0%;
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AZ119770
AZ119770.1 GI:7785028
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                                                                                                                                            Ouery Match
Best Local Similarity 100.
Matches 11; Conservative
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78 GCCTTAAGGGC 88
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DB 13; Length 115;

Score 11;

100.08;

Query Match

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                                                                                                                                                                                                                               AQ355689 24-JAN-1999 CITBL-E1-2538F8 TR CITBL-E1 Homo sapiens genomic clone 2538F8, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uppublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
1e1: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
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SEST51785 Gall bladder I Homo sapiens CDNA 5' end similar to similar
to prolylcarboxypeptidase, mRNA sequence.
AA345723
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calTech Human BAC Library D"
1 23 c 21 g 44 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.5e+03;
Mismatches 0;
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100.0%; Pred. No. 7.5e+03;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
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/clone="2538F8"
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AQ355689.1 GI:4182862
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GI:1141358
   Unpublished (1999)
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                   Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Rerick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, Coleman, T.A., Collins, E.J., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Husson, P., Kim, A.K., Kozak, D.L., Kusch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wig, J., Xu, C., Yu, G.L., Raser, C.M. and
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RPCI-23-479M23.TV RPCI-23 Mus musculus genomic clone RPCI-23-479M23
AZ123745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
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In (Dasses I to 140)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 140)
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/sex="female"
/dev_stage="adult, 25 yrs"
/note="Organ: gall bladder; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
59 c 4 others
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/db_xref="ATCC (inhost):147260"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter, J.C.
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ESM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 147)

1 (Lases 1 to 147)

Si Hilier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project

Contact: Wilson RK

Mashington University School of Medicine

4444 Forest Park Park Way, Box 850i, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson, wustl.edu

High quality sequence starts: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 selected DNA was cloned into the pBACe3.6 vector at the DCORI sites. The ligation products were transformed into BCORI electrocompetent cells (BRL Life Technologies). " 39 c 22 t
                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 479 row: M column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and ECORI Methylase. Size
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-479M23"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .140
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/sex="male"
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Best Local Similarity 100.
Matches 11; Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 149)
Mei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.

Pediatric Leukemia cDNA Sequencing Project
Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Eates, MC3-3320 Houston, TX 77030, USA
High quality sequence stops: 1
Source: IMAGE Consortium, Linn.
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyT not found
Seq primer: mil 3 - 40 forward
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE245846 149 bp mRNA EST 15-NOV-2000 TCBAP1E1938 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1938, mRNA
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/db_xref="taxon:9606"
/clone="TcBAp1938"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"
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100.0%; Pred. No. 7.5e+03;
clve 0; Mismatches 0;
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                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:3887458"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: clones@txccc.orq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative 0
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BE245846
BE245846.1 GI:9097594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GCCTTAAGGGC 112
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Chote-Vector: lambda pSB; Site_1: BamHI; Site_2: ECORI; First strand cDNA was primed with an anchored strand cDNA was primed with an anchored strand cDNA was primed with a BamHI-dc primer Strand was primed with a BamHI-dc primer Strand was primed with a BamHI-dc primer [5'AGAGAGTCGGATCCGGCCCGAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one cound of normalization. Library was constructed by Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N41203 158 bp mRNA EST 22-JAN-1996 HR179-F Adult heart, Clontech Homo sapiens cDNA clone R179-F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Waye Mary M.Y.
Department of Biochemistry
The Chinese University of Hong Kong
Rm 302C, Basic Medical Science Building, The Chinese University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 158)
Waye,M.M.Y., Cheung,H.K.Y., Lam,W.Y., Law,P.T.W., Lo,A.S.Y., Lui, V.W.Y., Luk,S.C.W., Tsui,S.K.W., Tung,C.K.C., Yam,N.Y.H., Liew,C.C. and Lee,C.Y.
Gene expression of adult human heart as revealed by random sequencing of cDNA library
Miani Winter BioTechnol. Symp. Proc. 6, 90 (1995)
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//lab_host="E. coli Y1090"
//note="Vector: Lambda gtll; Site_l: EcoRI; Site_2: EcoRI"
50 c 35 g 24 t
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Best Local Similarity 100.0%; Score 11; DB 11;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 11; Conservative 0; Mismatches 0;
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
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Email: b133723@vax.csc.cuhk.hk
Seq primer: GGTGGCGACGACTCCTGGAGCC.
Location/Qualifiers
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Tel: 8526096874
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/db_xref="taxon:9606"
/clone="R179-F"
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AQ012949.1 GI:3185514
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Best Local Similarity 100.
Matches 11; Conservative
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CIT-HSP-2300F24.TF CIT-HSP Homo sapiens genomic clone 2300F24, DNA
                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
110. Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
                                                                                                                TCBAPIE0434 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0434, mRNA
                                                                                                    15-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project=TCBA"
/sex="male"
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100.0%; Score 11; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 11; Conservative 0; Mismatches 0;
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/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_nost="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP0434"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 primer.
Location/Qualifiers
                                                                                                    mRNA
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                141 GCCTTAAGGGC 131
1 GCCTTAAGGGC 11
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1 (bases 1 to 165)

S Adams, W. D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

U. Other GSS: CIT-HSP-2300F24.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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3366 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
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; Pred. No. 7.5e+03;
0; Mismatches 0;
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/db_xref="GDB:7154476"
/db_xref="taxon:9606"
/clone="2300F24"
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organism="Mus musculus"
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                                                                                                          Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pcMv SPORT6; Site_1: Xba1, Site_2: Xho1, Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 172;
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Possible reversed clone: similarity on wrong strand
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4359
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100.0%; Pred. No. 7.5e+03;
iive 0; Mismatches 0;
                                                                                    Email: smith@email.marc.usda.gov
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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High quality sequence stop: 1.
Location/Qualifiers
1..181
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BACKWARD: GTTTCCCAGTCACGACG
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314 286 1810
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AI303597
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/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Ist strand cDNA was primed with an oligo(dT) primer was primed with an oligo(dT) primer and corganization of the pME18S-FL3 istanded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). AhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_inAdG:2365069"
/clone_lib="Scares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DHIOB"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP putification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGGG and 3' end primer GACCTGCAGACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1800916 182 bp mRNA EST 19-DEC-1999 wg14d07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2365069 3' similar to 9b:L10320 FRUCTOSE-1,6-BISPHOSPHATASE
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1 (bases 1 to 182).
NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1617 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                   /clone_lib="Sugano mouse liver mlia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1888798"
                                                                                                                                          /sex="female"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMAN);, mRNA sequence.
AI800916
AI800916.1 GI:5366388
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Best Local Similarity
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Length 185;

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                        A2075637.1 GI:7368534
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 199)
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                           1 GCCTTAAGGGC 11
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AZ075637/c.
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PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSP pool 1: 14502-147355, 147720-148103, 148872-149955, 15002 - 150407, 151176-152375 Soares NbHFF9 9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904-e. vector identified by cross_match with the -minscore 18
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 185)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
.G.L., Heaton,M.P., Laegreeid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                 100.0%; Score 11; DB 10; Length 182; 100.0%; Pred. No. 7.4e+03; Live 0; Mismatches 0; Indels
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BF61555 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF605530.1 GI:11705237
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/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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BACKWARD: GTTTTCCAGTCACGACG
Plate: 55 row: F column: 24
Seq primer: ATTTAGGTGACACTATAG.
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BF605530/c
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                      AZ075637 199 bp DNA GSS 31-MAR-2000
RPCI-23-408L19.TV RPCI-23 Mus musculus genomic clone RPCI-23-408L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 408 row: L column: 19
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                      Gaps
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Tel: 301 838 0200
Fax: 301 838 0208
                                                      Indels
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100.0%; Pred. No. 7.4e+03;
iive 0; Mismatches 0;
Score 11; DB 11;
Pred. No. 7.4e+03;
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                                                   0; Mismatches
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/clone_lib="RPCI-23"
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V00083 Artificial A49702 Sequence 8 U13846 pCM7 clonin J01753 Plasmid pBR

186203 AAP927 AA9702 XXU13846 SXYNPBR329 AS2306 AR027062 186195 A49695 A49696

AR038307 Sequence AR038321 Sequence I58596 Sequence 15 I58610 Sequence 17

AR038307 AR038321 158596 158610 AX180726 AR027070

AX027785

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A5226 Sequence 1 A8027062 Sequence 1 186195 Sequence 1 A49695 Sequence 1 A49696 Sequence 2 A77044 Sequence 2 A77044 Sequence 3 109267 Sequence 34 109267 Sequence 34 109268 Sequence 35 109268 Sequence 36 A08457 phfs 164 mRN 109252 Sequence 19 109251 Sequence 19 109251 Sequence 19 109254 Artificial

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ALIGNMENTS

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AR002333 Sequence AR018032 Sequence AR055698 Sequence AF087567 Cloning v

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AX027785 GI:10188633
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Result
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                                           January 17, 2002, 11:48:13 ; Search time 10436.3 Seconds (without alignments) 2252.560 Million cell updates/sec
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1 TGCCATGGGGGGGATTCTT......CAGCCTCTCCCACAGGTACC 1425
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

synthetic construct.

synthetic construct
artificial sequence.

1 (bases 1 to 11795)

Bollen,A., Jacobs,P., Jacquet,A., Haumont,M. and Massaer,M.G.
Varicella-zoster virus vaccines.
Patent: WO 0043527-A 4 27-JUL-2000;
SMITHKLINE BEECHAM BIOLOG (BE); BOLLEN ALEX (BE); JACOBS PAUL (BE); JACQUET ALAIN (BE); HAUMONT MICHELE (BE); MASSAER MARC GEORGES FRANCIS (BE)

Location/Qualifiers
1. 11795 /organism="synthetic construct" source FEATURES

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Button, D.R., Barbas, C.F. and Lerner, R.A.
Human neutralizing monoclonal antibodies to human immunodeficiency
virus
Patent: US 5804440-A 156 08-SEP-1998;
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Pred. No. 3.4e-117;
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Sequence 156 from patent US 5804440.
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2760 c 2957 q 3.
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6149 GTCGGAACAGGAGAGCGCACGAGGAGCTTCCAGGGGGGAAACGCCTGGTATTTTTAGT
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Burton, D.R., Barbas, C.F. and Lerner, R.A.
Human neutralizing monoclonal antibodies
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Patent: US 5804440-A 170 08-SEP-1998;
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Joly,E.
A bioluminescence resonance energy transfer (bret) fusion molecule
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1 (bases 1 to 13254)

Burton, D. R., Barbas, C.F. and Lerner, R.A.

Human neutralizing monoclonal antibodies to human immunodeficiency
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                                                                               6449 GTGTAGCCCTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 6390
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                                 7106 GTCGGAACAGGAGAGAGAGAGAGAGAGTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
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               GTCGGAACAGGAGGCCCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
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                                                                                                                                                 1132 CGGAGCCTATGGAAAAACGCCAGCAACGCGGGGGG 1169
                                                                                                                                                                   1 (bases 1 to 13254)
Burton, D.R., Barbas, C.F. and Lerner, R.A.
Human neutralizing monoclonal antibodies
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1. .13254
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3559 c 3251 q
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Sequence 156 from patent US
158596 15:2477834
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1 (Cases 1 to 1905)
Legoux,R., Maldonado,P. and Salome,M.
Legoux,R., Maldonado,P. and Salome,M.
Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
patent: US 5700665-A 9 23-DEC-1997;
Location/Qualifiers
1.1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
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                                            772 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTTTACCGGGTTG
                                                       Length 1905;
                                                                                                                                                                                                                                                                                                                                                                                                  PAT
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Pred. No. 6.5e-117;
0; Mismatches 2;
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493 c 442 q
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nilarity 99.6%;
Conservative 0
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Matches 455; Conserv
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TITLE
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Legoux, R., Maldonado, P. and Salome, M.
Legoux, R., Maldonado, P. and Salome, M.
Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
Patent: US 5855142-A 9 05-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGTAAGCGGCAGGGTCGGAACAGGAGGACGCACGAGGGAGCTTCCAGGGGGAAACGCCT 1057
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                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            5043 CGGTAAGCGGCAGGGTCGGAACAGGAGGGCCACGAGGGAGCTTCCAGGGGGAAACGCCT
                                                                                                                                                                                                                758 CTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGT
                                                                                                                                                                                                                            GTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAA
                                                                /note="DNA sequence for Rluc-PKA-EYFP construct"
1685 c 1685 g 1647 t
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Pred. No. 5e-117;
0; Mismatches 8; Indels
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31.8%; Score 453.8; DB 6;
Best Local Similarity 99.6%; Pred. No. 6.5e-117;
Matches 455; Conservative 0; Mismatches 2;
                                           /organism="synthetic construct"
/db_xref="taxon:32630"
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  Patent: WO 0146694-A 6 28-JUN-2001;
Biosignal Packard Inc. (CA)
Location/Qualifiers
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493 c 442 g
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AR027070
AR027070.1 GI:502777
                                                                                                                            31.9%;
98.3%;
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Unclassified.
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Best Local Similarity
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2094 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 2035
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                                         Gaps
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
unclassified Orthomyxoviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT
Score 453.8; DB 12;
Pred. No. 6.5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 453.8; DB 6;
Pred. No. 6.5e-117;
0; Mismatches 2;
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Sequence 8 from Patent WO9610641.
A49702 GI:2303038
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                                         Mismatches
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Hobom,G., Neumann,G. and Menke,A.
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1001 c 1004 g
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1. .4023
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99.6%;
                                     Matches 455; Conservative
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                     Similarity
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Matches 455;
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/protein_id="CAA23425.1"
/protein_id="RAA23425.1"
/db_xref="G1:808934"
/translation="MRTRSRYNPLWPPSPARFATWSHYRLRDHGDHTRPVDPLRR
THRGRHHRRHRGGGNRYRRHRWGRGSPLRAHERJERRGYGGRPYAGGLLGAISLH
APFLAAAVLNGLLLGGFLMQESHKGERRPWPLRAFNPVSSFRWARGMIVAALMTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
QLGGSLAALTSLTSITGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAWSR
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SYPTEKHLTDGMTYRELCSAAITMSDNTAANLLTTTGGGEVELTAFLHNGDHYTRL
DRWEPELNRA I PINDENTTWARAMATILRKLLTGELLTASROOLIDMMEARYAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                    ARF327 3273 bp DNA circular SYN 17-MAY-1995 Artificial cloning vehicle pBR327, derived from pBR322. The sequence was not resequenced but deduced from the pBR322 sequence. Contains the reading frames for ampicillin resistance (Apr) and tetracycline resistance (Tcr) and an origin of replication.
                                                           1011
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                                                                                                                                                                                                               1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
                                                                                                                                                       artificial sequence.

1 (bases 1 to 3273)
Soberon,X., Covarrubias,L. and Bolivar,F.
Construction and characterization of new cloning vehicles. IV.
Deletion derivatives of pBR322 and pBR325
Gene 9 (3-4), 287-305 (1980)
                                                                                                                                                                                                                                   158 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 99
                   ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                 1012 GTCGGAACAGGAGGGCGCACGAGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
 v00083.1 G1:58119
circular; cloning vector; drug resistance gene; origin of
replication; plasmid.
synthetic construct.

    .3273
/organism="synthetic construct"
/db_xref="taxon:32630"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="tetracycline resistance"
                                                                                                                                                                                                                                                                                                          CGGAGCCTATGGAAAAACGCCAGCAACGCGGCCCGAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2205. .3065)
/note="ampicillin resistance"
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/db_xref="GI:808935"
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/transl_table=11
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Close, T.J. and Rodriguez, R.L.
Construction and characterization of the chloramphenicol-resistance
gene cartridge: a new approach to the transcriptional mapping of
extrachromosomal elements
Gene 20 (2), 305-316 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoterless. The cat gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCM7: A promoter analysis, chloramphenicol acetyltransferase gene
cartridge vector
Submitted (19-AUG-1994) James A. Malone, International Technical Services, Molecular Biology Reagents Division, Pharmacia Biotech Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA Location/Qualifiers
                                                                                                                                                             1011
                                                         1974 GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGCTGACGGGGGTTGAACGGGGGGTTCGTGC 1915
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Alton'N.K. and Vapnek,D.
Nucleotide sequence analysis of the chloramphenicol resistance
Lransposon Tn9
Nature 282 (5741), 864-869 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-1994
                                                                                               ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                      952 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                      1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG
                                                                                                              1012 GTCGGAACAGGAGGGCGACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                         GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chloramphenicol acetyltransferase; promoter analysis;
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//Organism="unidentified cloning vector"
/db_xref="taxon:45;96"
/lab_host="Escherichia coli"
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                                                                                                                                                                                                                                                                                                                                             /gene="cat"
/note="The cat gene in pCM7 is
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA circular complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           artificial sequence; vectors.
1 (bases 1 to 4060)
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67. .726
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/translation="MEKKITGYTTVDISQSHRKEHFBAFOSVAQCTYNQTVOLDITAF
LKTVKKNKHKFYPAFIHILARLANAHPEFRMAMKDGELVIMDSVHPCYTVFHEGTETF
SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILESFRPERFPPMSFFKVLLCGAVLSRVDAGOEGGLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCASAITWSDNTAANLLITIGGRFKELTAFTHNMGHVTRL
DRWBFELNEA IPNDSRCTTWPAAMATTLRKLLTGELLTLASROQLIDWMEAVVAGFL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATWDERNRQIA
                                                                                                                                                                                                                                                                                             /note="plasmid origin of replication; base 2233 represents the first base of the newly synthesized strand"
                                                                                                                                                                                                                                 ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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  as a HindIII fragment'
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Pred. No. 6.5e-117;
0; Mismatches 2;
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                                                       /codon_start=1
/transl_table=11
/product="chloramphenicol at
/protein_id="AAA57080.1"
/db_xref="G1:595697"
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/protein_id="AAA57081.1"
/db_xref="G1:595698"
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/gene="bla"
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/citation=[2]
/citation=[3]
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                                                                                                 cloning vector; complete genome.
plasmid pbi329 from E.coli k-12.
unidentified cloning vector
artificial sequence; vectors.
1 (bases 1 to 4150)
Covarruthas,L. and Bolivar,F.
Construction and characterization of new cloning vehicles: Vi. plasmid pbR329, a new derivative of pbR328 lacking the 482-base-pair inverted duplication
6ene 17, 79-89 (1982)
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99.6%; Pred. No. 6.5e-117;
tive 0; Mismatches 2;
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/db_xref="taxon:45196"
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                                                      Plasmid pBR329, complete genome. J01753
                                                  DNA
                                                 4150 bp
                                                                                      J01753.1 GI:208964
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12-DEC-1997

PAT

Sequence 1 from Patent EP0725140. A52326

A52326

A52326/c LOCUS DEFINITION ACCESSION VERSION

A52326.1 GI:2851987

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338. .762
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                                                                                       proteins from prokaryotic
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/note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"
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/note="TERMINATEUR DU GENE 10 DU PHAGE T7"
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Anote-"GENE CODANT POUR LE REPRESSEUR DE
2506. .4410
/note="SEQUENCE DE PBR 327"
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                                                          Legoux, R., Maldonado, P. and Salome, M. Process of extraction of periplasmic proteins microorganisms in the presence of arginine patent: EP 0725140-A 1 07-AUG-1996; SANOFI SA (FR)

Cher publication SK 10696 960914 other publication C2 9600290 960914 other publication PB 8242879 960921 other publication PI 960427 960801 other publication PI 312343 960805 other publication PC 316382 960805 other publication R2 722997-960801 other publication R2 2169382 960801 other publication R4 224496 960808 other publication R4 224496 960808
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Pred. No. 6.5e-117;
0; Mismatches 2;
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    /organism="unidentified"
    /db_xref="taxon:32644"
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Legoux, R., Maldonado, P. and Salome, M.
Method for the extraction of periplasmic pr
microorganisms in the presence of arginine
Patent: US 5856142-A 1 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                              Score 453.8; DB 6;
Pred. No. 6.5e-117;
1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGG 1168
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1 (bases 1 to 4410)
Legoux, R., Maldonado, P. and Salome, M.
Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
Patent: US 5700665-A 123-DEC-1997;
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Pred. No. 6.5e-117;
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                                                                                                                                            /organism="unknown"
1142 c 1096 g
                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                31.8%;
99.6%;
                                                                                                                                                                                                                                                                 Best Local Similarity 99.6
Matches 455; Conservative
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Search completed: January 17, 2002, 11:49:01 Job time: 17153 sec

10-JUN-1998

PAT

186195 4410 bp DNA Sequence 1 from patent US 5700665. 186195

DEFINITION

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186195.1

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SOURCE ORGANISM

KEYWORDS

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Complete sequence
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Plasmid pHS 164.
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Universal reporter
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Plasmid pSP72. Es
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Plasmid BGINV.
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/note= "combined splice and polyA sequences"
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/note= "ColE1 origin of replication"
1177..1425
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/note= "stuffer sequence"
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/note= "RANTES promoter"
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/note= "SupF gene"
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Chimeric - Escherichia coli.
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                                                                                                                                                                                                  1425
1 TGCCATGGCGCGGATTCTTT......CAGCCTCTCCCACAGGTACC 1425
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| SIDS2/gcgdata/geneseq/geneseqn/Nal981.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqn/Nal984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/Nal985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/Nal995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/Nal991.DAT:*
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 1.0
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Score

Result No.

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Plasmid pITL comprises a base vector for novel humanised polynucleotide vectors. Such vectors comprise a human-derived polynucleotide vectors. Such vectors comprise a human-derived promoter or manmalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site (see AAV2175-36), which accepts CDNA products from RT-PCR cloning. They also contain minimal non-human components, such as a replication of the vector, is well as human-derived are necessary for production of the vector, as well as human-derived spid polyA sequences (see AAV21723). The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and appropriately presented on antigen presenting cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                             Claim 14; Page 29-30; 125pp; English.
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                                                97WO-US14306
                                                                           96US-002393
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Best Local Similarity 100.
Matches 1425; Conservative
                                                                                                                                         Nelson PJ;
                                                                                                                                                                    WPI; 1998-159552/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1425
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              19-FEB-1998
                                                                                                          SO ( HSSO)
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GCCACGCTTCCCGAAGGGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACA 1020
                                                                                                                                                                                                                                                                                                        GGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGG 1080
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                                                                                                                             720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGCCCCTCAACTGGCCCTATAAAGGGCCAGCCTGAGCTGCAGAGGATTCCTGCAGAGG 1380
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                                                                                                                                                                                                                                                                960
                                                                                                                                                                                                                                                                             901 agcttggagcgaacgacctacaccgaactgagatacctacagcgtgagcattgagaaagc 960
AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGGGTGAGCATTGAGAAAGC
                        TAAGCTTGATATCGAATTCTTTTCTCAACGTAACACTTTACAGCGGCGCGTCATTTGATAT
                                                        GATGCGCCCCGCTTCCCGATAAGGGAGCAGGCCAGTAAAAGCATTACCCGTGGTGGGGTT
                                                                                         CCCGAGCGGCCAAAGGGAGCAGACTCTAAAATCTGCCGTCATCGACTTCGAAGGTTCGAAT
                                                                                                  CCTTCCCCCACCACCATCACTTTCAAAAGTCCGAAAGAATTCCTGCAGCCCGTGTAGCCG
                                                                                                                                                           TAGITAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATC
                                                                                                                                                                                            CTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA
                                                                                                                                                                                                    CGATAGTTACCGGATAAGGCGCCAGCGGTCGGGCTGAACGGGGGGGTTCGTGCACACAGCCC
                                                                                                                                                                                                                                      GTGAGGGAGAGACAGAGACTCGAATTTCCGGAGCTATTTCAGTTTTCTTTTCCGTTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAATTTCACTTATGATACCGGCCAATGCTTGGTTGCTATTTTGGAAACTCCCCTTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAAGACAGCACGTGGACCTCGCACAGCCTCCCCACAGGTACC 1425
                                        481
       421
                        481
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standard; cDNA; 2125

AAV21727 AAV21727;

RESULT
AAV21727
ID AAV2
XX
AC AAV2

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- comprising human derived promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence, generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other component
                                                                                                                                                                                                                                                                                                                                                                                                                   sequence acceptance site, used for the production of vaccines
                                                                                                                                                                       polyA sequences"
                                             Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu; human; HER-2/neu; C-erbB-2; breast cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2125 BP; 449 A; 650 C; 598 G; 428 T; 0 other;
                                                                                                                                                                                                                              replication
                                                                                                                                                             /*tag= b
/note= "combined splice and
                                                                                                                                          human HER-2/neu
                                                                                                                                                                                                                   /*tag= d
/note= "ColE1 origin of :
1877..2125
                                                                                                                                                                                                                                                          promoter'
                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 41-42; 125pp; English
                                                                                                              Location/Qualifiers
13..921
                                                                                                                                                                                                  gene"
                                                                                                                                                                                                                                                                                                                                                                                                             Humanised polynucleotide vectors
                                                                                                                                                                                                                                                       /note= "RANTES
                           Humanised vector pITL-hHER/neu
                                                                                                                                                                                       /*tag= c
/note= "SupF
                                                                         Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                  96US-0023931
                                                                                                                               /*tag= a
/product= 1
922..1181
                                                                                                                                                                                                        1412..1864
        (first entry)
                                                                                                                                                                              1195..1401
                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                       Nelson PJ;
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-159552/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the vectors
                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                14-AUG-1997;
        17 - AUG - 1998
                                                                                                                                                                                                                                                                           WO9806863-A1
                                                                                                                                                    polyA_site
                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       Welson EL,
                                                                                                                                                                                                                                      promoter
                                                                                                              Key
                                                                                                                                                                                CDS
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Plasmid pITL-hHER2/neu comprises base vector pITL (see AAV21724) and a human HER-2/neu nucleic sequence. pITL-hHER2/neu was used to evaluate the toxicity of anti-tumour vaccination in rats, and in phase I and phase II trials to evaluate polynucleotide vaccination in advanced breast cancer. Novel humanised vectors, which can be based on pITL, comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells but are capable of extended stable expression of the target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     components
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                                                                    gccttaagggccatatggtgagtggatgccttgaccccaggcggggatgggggagacctg 981
                                            GCCTTAAGGGCCCATATGGTGAGTGGCTTGACCCCAGGCGGGGATGGGGGAGACCTG
                                                         ö
  Length 2125;
                        Indels
                       ;
 DB 19;
Score 1203; 1
Pred. No. 0;
                        Mismatches
                        .
0
  84.48; 8
                        Conservative
           Similarity
Query Match
Best Local Simi
Matches 1203;
                                                                  922
                                            223
                                                             g
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1461 1581 1641 agcggcagggtcggaacaggagagcgcacgagggagcttccagggggaaacgcctggtat 1761 TTTTCTTTTCCGTTTTGTGCAATTTCACTTATGATACCGGCCAATGCTTGGTTGCTATTT 1302 attacccgtggtggggttcccgagcggccaaagggagcagactctaaatctgccgtcatc 1341 gacttogaaggttogaatocttococcaccaccatcactttcaaaagtocgaaagaatto 1401 762 ctgcccgggtgggatcctgtgacccctccccagtgcctctcctggccctggaagttgcc ACTCCAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTCTGACTAG CTGCAGCCCGTGTAGCCGTAGTTAGGCCACCTCTCAAGAACTCTGTAGCACCGCCTACA tacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtctt <u> AGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTAT</u> CTTTATAGTCCTGTCGGGTTTCGCCACCTCGACTTGAGCGTCGATTTTTGTGATGCTCG TCAGGGGGGGGGGAGCCTATGGAAAAACGCCAGCAACGCGGGGGCCCGGGGGATCCGGAGAGCTC ACTCTAGATGAGAGCAGTGAGGGAGAGACAGAGACTCGAATTTCCGGAGCTATTTCAG ATTACCCGTGGTGGGGTTCCCGAGCGGCCAAAGGGAGCAGACTCTAAATCTGCCGTCATC GACTTCGAAGGTTCGAATCCTTCCCCCACCATCATTCAAAAAGTCCGAAAGAATTC TACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTT ACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGG TGGAAACTCCCCTTAGGGGATGCCCCTCAACTGGCCCTATAAAGGGCCAGCCTGAGCTGC CTGCCCGGGTGGGATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCC 403 1102 1162 1222 1282 643 1342 703 1402 1462 823 1522 1582 1642 1003 1702 1063 1123 1822 1243 1942 283 463 1762 1183 1882 1303 2002 343 1042 523 583 763 883 943 qq QQ δ qq qq δy g ò Dp q δ g δy g ò 8 ò g δ g Ω g ď q 셤 ò g ŏ g à q ÓΥ δŽ δ ò

non-replicating in mammalian cells but are capable of

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Humanised polynucleotide vectors – comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pITL-GFP comprises base vector pITL (see Anversor, humanised green fluorescent protein (GFP) reporter sequence (see AAV21725). Novel humanised vectors comprise a human-derived promoter or manmalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. pITL-GFP was used to examine the kinetics of expression of a reporter sequence from such vectors in an animal model (Fisher 344 rats). Toxicity from such vectors in an animal model (Fisher 344 rats). Toxicity from such vectors in an animal model (Fisher 344 rats).
                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "combined splice and polyA sequences"
                                                                                                                                                                                                                                                                                                                                                                      replication"
                                                                                                                                                                                                                                                                                   /product= green fluorescent protein
                                                                                                                                                                                tumour; antigen; plasmid pITLGFP;
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 33-34; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                            /*tag= d
/note= "ColE1 origin
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 /*tag= c
/note= "SupF gene"
                                                                                                        BP
                                                                                                     AAV21726 standard; cDNA; 1911
                                                                                                                                                                                                                           - Aequorea victoria
                                                                                                                                                                                                        Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US14306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0023931
                                                                                                                                                                                       green fluorescent protein;
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                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                            1663..1911
                                                                                                                                                            Humanised vector pITL-GFP.
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                                                                                                                                                                                                                                                                                                                       981..1187
                                                                                                                                                                                                                                                                                             720..967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-159552/14.
                                                                                                                                                                               vaccine;
                                     ACC 1425
                                                       2122 acc 2124
                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                WO9806863-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-1996;
                                                                                                                                          17-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1998
                                                                                                                                                                                                                                                                                            polyA_site
                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson EL,
                                                                                                                                                                                                                   Chimeric
Chimeric
                                                                                                                        AAV21726;
                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                Vector;
                                      1423
                                                                                             AAV21726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1196 cogtgtagccgtagttaggccaccacttcaagaactctgtagcaccgcctacatacctcg 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1316 tggactcaagacgatagttaccggataaggcgcagcggtcgggctgaacggggggttcgt 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTCGGAACAGGAGGCGACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATA 1069
                                                                                                                                                                                                                                                                                                                                                                          290 AGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGTGAGTAGTGACTGCCCG 349
                                                                                                                                                                                                                                                                                                                                                                                                                  835
                                                                                                                                                                                                                                                                                                                                                                                                                                                        409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggtcggaacaggagagagcacgagggagcttccagggggaaacgcctggtatctttata 1555
                                                                                                                                                                                                                                                                                             230 GGGCCATATGGTGAGTGCATGCCTTGACCCCAGGCGGGATGGGGGGAGACCTGTAGTCAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                             Gaps
stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGGGATCCCTGTGACCCTCCCCAGTGCCTCTCCTGGCCTGGAAGTTGCCACTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      836 ggtgggatccctgtgacccctccccagtgcctctcctggccctggaagttgccactccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1076 9tggtggggttcccgagcggccaaagggagcagactctaaatctgccgtcatcgacttcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTTGTCTGACTAGGTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATAATATTATAAGCTTGATATCGAATTCTTTCTCAACGTAACACTTTACAGCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTTGATATGATGCGCCCCGCTTCCCGATAAGGGAGCAGGCCAGTAAAAGCATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGTGGGGTTCCCCGAGCGGCCAAAGGGGAGCACTCTAAAATCTGCCGTCATCGACTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGCTAATCCTGTTACCAGTGGCTGCTGCCGGTGACGTCGTCGTGTCTTACCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 TGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCCTGAACGGGGGGGTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACACACCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1070 GTCCTGTCGGGTTTCGCCACCTCTGAGCGTCGATTTTTGTGATGCTCGTCAGGGG
                                                                                                                                                                                                                       Length 1911;
                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                          Sequence 1911 BP; 474 A; 514 C; 511 G; 412 T; 0 other;
                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                     Score 1194.4;
Pred. No. 0;
                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                     83.8%;
99.9%;
                                                                                                                                                                                                                                       Best Local Similarity 99.9
Matches 1195; Conservative
                                                                                                                                                                                                                     Query Match
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                                                                                            TCCCCTTAGGGGATGCCCCTCAACTGGCCCCTATAAAGGGCCAGCCTGAGCTGCAGAGGAT 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                  TCCTGCAGAGGATCAAGACAGCACGTGGACCTCGCACAGCCTCTCCCACAGGTACC 1425
                                                                                                                                                         gtectgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcagggg
                                        TICCGITITIGICCAAITICACTIAIGATACCGGCCAAIGCITGGITGCIAITITIGGAAAC
                        GGCGGAGCCTATGGAAAAACGCCAGCAACGCGGGCCGGGGGATCCGGAGAGCTCTAG
                                                      ATGAGAGAGCAGTGAGGGAGACAGACTCGAATTTCCGGAGCTATTTCAGTTTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pITL-A comprises a base vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH 10-beta/P3 is deposited as ATCC 98401. Novel vectors comprise
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                                                                                                                                                                                                                                                                       Vector; vaccine; tumour; antigen; plasmid pITL-A;
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/note= "RANTES promoter"
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/note= "ColE1 origin
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                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/*tag= c
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Chimeric - Escherichia coli
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                                                                                                                                                                                                                                                       Humanised vector pITL-A.
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                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTTGATATCGAATTCTTTCTCAACGTAACACTTTACAGCGGCGCGTCATTTGATATGA 542
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                                                                                                                                                                                     are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response responsed in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
                      in mammalian target tissue and cells and a sequence acceptance site (see AAV21735-36) which accepts CDNA products from RT-PCK cloning. They also contain minimal non-human components, such as a replication origin (see AAV21715) and selectable marker gene (see AAV21717-18) tare necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are nor-replicating in mammalian cells but are capable of extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agcagccggcgctttactggcacttcaggaacaagcgggcgccttaagggccatatggtg
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promoter or mammalian homologue which is functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1547 BP; 344 A; 408 C; 425 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 490.4; DB 19;
Pred. No. 9.4e-126;
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Best Local Similarity 62.8%;
Matches 984; Conservative
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                                                                        820 tcgtgcgctctcctgttccgaccctgccgcttaccggatacctgtccgcctttctccctt
                                                                                                      933 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCC---------
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                                                      813 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG
                                                                                           873 CTGAACGGGGGGTTCGTGCACACACCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG
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iniluenza virus; antigen; specific; immune response; nucleoprotein; hemagglutinin; polymerase; matrix protein; non-structural protein; human; vaccine; ds.

(first entry)

31-MAY-1995

Expression vector VlJneo.

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The sequences given in AAQ74206-08 represent expression vectors which were used for the expression of influenza virus genes. VIJ contains the contains the amps gene and ViJneo contains the kank gene in the same orientation. DNA constructs such as these, containing the influenza virus genes are capable of inducing the expression of an antigenic influenza virus gene product which induces a specific immune response upon introduction of the DNA construct into animal tissue in vivo and resultant uptake of the DNA construct by cells which express the encoded influenza gene. The encoded influenza virus gene encodes nucleoprotein, hemaglutinin, polymerase, matrix or non-structural human influenza virus gene products. The virus gene is operably linked to one or more control sequences for incorporation in a vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15; Length 3553;
                                                                                                                                                                                                                                                                                                                                     Parker SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus genes – fo
influenza virus
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                                                                                                                                                                                                                                                                                                                                  Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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Pred. No. 3.7e-117;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide vaccine comprising influenza vaccination against more than one strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 105-07; 171pp; English.
                                                                                                                                                                                                                                                                                                                                  Liu MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match . 32.3%;
Best Local Similarity 97.5%;
Matches 467; Conservative
                                                                                                                                       94WO-US02751
                                                                                                                                                                                        93US-0032383
                                                                                                                                                                                                                 93US-0089985
                                                                                                                                                                                                                                                                                                                                  Dwarki VJ,
                                                                                                                                                                                                                                                             MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                      Ulmer JB;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-317017/39
                                                                                                                                                                                                                                                                                         (VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                                                  Donnelly JJ;
                                                                                                                                          14-MAR-1994;
                                                                                                                                                                                      18-MAR-1993;
08-JUL-1993;
                                              WO9421797-A
                                                                                             29-SEP-1994
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Synthetic.
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Vector pEe6FFBHCDR20 (AAT50962) comprises the TFBHCDR20 CDR-grafted heavy chain gene inserted into vector pEe6hCMV-BgIII. It encodes a CDR-grafted heavy chain (AAM10232) in which CDRs (see also AAW10222-24) from the mouse anti-tissue factor monoclonal antibody FFB-5G9 are grafted into a human KOL antibody framework. The heavy chain constant region is derived from human IgG4. Humanised antibodies are obtd. by cotransfecting a host cell with vectors encoding the CDR-grafted heavy and light chains (see also AAW1023). These antibodies are capable of inhibiting human tissue factor and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3329 GTGTAGCCGTAGTTAGGCCACCACCACTTCAAGAACTCTGTAGGCACCGCTACATACCTCGCT 3270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 TGAGAAAGCGCCACGCTTCCCGAAGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to treat e.g. intravascular coagulation, arterial restenosis
                                                                                                                                                                                                                                                                                                              CDR-grafted antibody capable of inhibiting human tissue factor used in the treatment of thrombotic disorders, e.g.intravascular coagulation, arterial restenosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.9%; Score 454.8; DB 18; Length 7073; Best Local Similarity 99.6%; Pred. No. 1.2e-115; Matches 456; Conservative 0; Mismatches 2; Indels 0;
                                          /*tag= q
/note= "Pst-1m fragment of hCMV contg. middle
/note= "XmnI-HindIII fragment of ColEl-based plasmid pCT54"
4886..7022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7073 BP; 1673 A; 1925 C; 1778 G; 1697 T; 0 other;
                                                            intermediate early promoter'
                                                                                       /*tag= r
/note= "pSP64 polylinker"
                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 74-80; 142pp; English.
                                                                                                                                                                                                                                                     Zivin RA;
                                                                                                                                                                            96WO-US09287
                                                                                                                                                                                                                           NOSNHOL & NOSNHOL ( CHOL)
                                                                                                                                                                                                                                                    Joliffe LK, Pulito VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and arteriosclerosis.
                                                                                                                                                                                                                                                                            WPI; 1997-099935/09.
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  2002 GATTTTGTGATGCTCGTCAGGGGGGGGGGCGAACCTATGGAAAAACGCCAGCAACGCGGCC 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "BQII-XmnI fragment of pSP64 beta-lactamase provides ampicillin resistance to transformed bacteria"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= n
/note= "fragment of pBR328 (nt 375-650, 1426-2422)
contains ColEl replication origin"
                                                                                                                                                                                                                                                                                                                                                    /function= TF8HCDR20 CDR-grafted heavy chain gene
                                                                                                                                                                          Tissue factor; complementarity determining region; CDR;
humanised antibody; monoclonal antibody; TF8-5G9; coagulation;
thrombosis; restenosis; arteriosclerosis; therapy;
pEe6TF8HCDR20; vector; ss.
                                                                                                                                                 TF8-5G9 CDR-grafted heavy chain gene in pEe6TF8HCDR20
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/note= "CDR-grafted variable region"
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note= "human IgG4 CH3 domain"
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/note= "human IgG4 CH1 domain"
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                                                                                                                                                                                                                                                                                         human cytomegalovirus strain AD 169
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/note= "human IgG4 intron
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1268..1594
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function= Kozak sequence
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'note= "human IgG4 hinge"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                          AAT50962 standard; DNA; 7073 BP
                                                                                                                                                                                                                                    Chimeric Mus sp.;
Chimeric Homo sapiens;
Chimeric Escherichia coli;
Chimeric simian virus 40;
Chimeric human cytomegalovir
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 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
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740 early promoter"
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/note= "includes polyA signal, ColEl replication
origin and amplicillin resistance genes"
3285..5736
                                                                                                                                                            Tissue factor; complementarity determining region; CDR; humanised antibody; monoclonal antibody; TFR-5G9; coagulation; thrombosis; restenosis; arteriosclerosis; therapy;
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                                                                                                                                                                                                                                                                                      /product= TFBLCDR3 CDR-grafted heavy chain
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/note= "includes hCMV middle intermediate
promoter and pSP64 polylinker"
                                                                                                                                           TF8-5G9 CDR-grafted light chain gene in pEel2TF8LCDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .-- Dase 4324 is given as n in the specification"...7864
                                                                                                                                                                                                                                                                                                                                                       /product= CDR-grafted variable region 393..710
                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/product* human kappa constant region
711..753
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "includes CHO glutamine syn
under control of the SV40
                                 1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGGG 1169
                                          2909 CGGAGCCTATGGAAAAACGCCAGCAACGGGGCCGGAGG 2872
                                                                                                                                                                                                           Chimeric - Homo Sapiens.
Chimeric - Escherichia coli.
Chimeric - Simian virus 40.
Chimeric - Human cytomegalovirus strain AD 169.
Chimeric - Cricetus cricetus.
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                                                                                                                                                                                                                                                                                                               /function= "Kozak sequence'
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1..759
/*tag= a
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/note= "base 4324
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                                                                                           AAT50963 standard; DNA; 7864
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                                                                                                                                                                                                                                                                                                  Vector pEel2TFBLCDR3 (AAT50963) comprises the TFBLCDR3 CDR-grafted light chain gene inserted into vector pEel2. It encodes a CDR-grafted light chain (AAM10233) in which CDRs (see also AAW10225-27) from the mouse anti-tissue factor monoclonal antibody FTF8-5G9 are grafted into a human REI antibody framework. The constant region is from the human kappa C region. Humanised antibodies are obtd. by cotransfecting a host cell with vectors encoding the CDR-grafted light and heavy (see also AAW10232) chains. These antibodies are capable of inhibiting human tissue factor and can be used to treat e.g. intravascular coagulation, arterial restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1012 GTCGGAACAGGAGGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
                                                                                                                                                                               CDR-grafted antibody capable of inhibiting human tissue factor used in the treatment of thrombotic disorders, e.g.intravascular coagulation, arterial restenosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7864 BP; 2020 A; 1925 C; 1850 G; 2068 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.9%; Score 454.8; DB 18;
99.6%; Pred. No. 1.2e-115;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132 CGGAGCCTATGGAAAAACGCCAGCAACGCGGGCCGGGGG 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1308 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCCGAGG 1271
                                                                                                                                                                                                                                                                 Claim 22; Page 84-89; 142pp; English.
                                                                                  RA;
                                                                                  Zivin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA59345 standard; DNA; 11795
95US-0480120
                                      NOSNHOL & NORNHOL ( THOL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                             Pulito VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arteriosclerosis.
                                                                                                                    WPI; 1997-099935/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                            P-PSDB; AAW10233
07-JUN-1995;
                                                                             Joliffe LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA59345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          807
                                                Varicella Zoster Virus; VZV; gE protein; chicken pox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                  protein and a (chickenpox) or
                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a fusion protein, which comprises a Varicella Zoster Virus (VZV) gE protein or an immunologically active fragment, fused to a different protein of VZV. The fusion protein or nucleic acids encoding it can be used to prevent or ameliorate Varicella (chicken pox) or Zoster (shingles) infections. The present sequence represents the plasmid pNIV4801, evector which is used to express fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCGGAACAGGAGGGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGGAACAGGAGGGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11795 BP; 2917 A; 2760 C; 2957 G; 3161 T; 0 other;
                                                                                                                                                                                                                                                                Massaer MGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                 Fusion protein comprising Varicella Zoster Virus gE
different VZV protein useful for treating Varicella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 454.8; DB 21
Pred. No. 1.4e-115;
0; Mismatches 2;
                                                                                                                                                                                                                                                              Jacquet A,
                         Nucleotide sequence of plasmid pNIV4801.
                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 27-34; 60pp; English.
                                                                                                                                                                                                                                                              Jacobs P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.9%;
99.6%;
                                                                                                                                                                                 17-JAN-2000; 2000WO-EP00352.
                                                                                                                                                                                                           99GB-0001254
(first entry)
                                                              shingles; NS1 protein; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 456; Conservative
                                                                                                    Varicella Zoster Virus
                                                                                                                                                                                                                                                              Haumont M,
                                                                                                                                                                                                                                                                                     WPI; 2000-505841/45.
                                                                                                                                                                                                                                                                                                                                          Zoster (shingles)
                                                   protein;
                                                                                                                            40200043527-A1
07-NOV-2000
                                                                                                                                                                                                           20-JAN-1999;
                                                                                                                                                       27-JUL-2000
                                                                                                                                                                                                                                                            Bollen A,
                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                Fusion
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This sequence represents the nucleotide sequence of the pEEL2 vector, pEel2 Combo BM 12, which contains the bl2 heavy and light chain genes. The pEEL2 vector has a human CMV promoter for expression of the light chain, a polylinker to provide cloning sites, and a polyadenylation signal for termination of transcription. The vector also contains the GS selectable marker gene whose expression is controlled by an SV40 early promoter at the 5' end of the GS gene, an intron, and a polyadenylation signal at the 3' end of the GS gene. A heavy chain cassette comprising the HCWV promoter, enhancer elements, heavy chain gene and polyadenylation signal were removed from the pEEG vector and inserted into the pEEL2 vector to generate the combinatorial construct containing both the bl2 light and heavy chain genes. The vector pEel2 combo BM 12 was used to transfect GNO cells and an antibody, bl2, was expressed. The resulting antibody has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 mg of antibody/ml. The MAD may be used for determining immunocompetence of a human anti-HIV antibody and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           772 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb; HIV; human immunodeficiency virus; glycoprotein; gpl20; clone; virus infectivity assay; precursor gpl60; immunocompetence; human; anti-HIV antibody; detection; HIV infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody binding to V1/V2 loop of HIV gpl20 - used in passive immuno:therapy and detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.9%; Score 454.8; DB 17; Length 13254; 99.6%; Pred. No. 1.5e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCGGGGG 1169
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of pEe12 Combo BM 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 276-285; 366pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lerner RA;
                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                   RESULT 9
AAT40915/c
ID AAT40915 standard; DNA; 13254
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-179601/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9602273-A1
                                                                                                                                                                                                                                                                                                                                                              29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sarbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                AAT40915;
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chain immunoglobulin amino acid sequence;

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This sequence represents a polynucleotide used in the preparation of the antibodies of the invention. The invention relates to the production of an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than for gymunor the production of the antibody comprises:

(a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAY98206) and a second polynucleotide encoding a light
6389 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTTTACCGGGTTG 6330
                                                                                                                                             1011
                                                                                                                                                                                                                                                       1131
                                                                                                                                                                                                   1071
                                                                                                                                                                                                                                                                                 6030
                           Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are specific for glycoprotein-120 -
                                                                                 892 ACACAGCCCAGCTTGGAGCGAACGACCTACAGCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                             CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG
                                                                                                                                                                                                                                                                 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                                              GTCGGAACAGGAGGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; anti-HIV monoclonal antibody; glycoprotein-120; human immunodeficiency virus type 1; HIV-1; infectivity titre; passive immunotherspy; reduce severity; HIV-induced disease; immunocompetence; active immunisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pEe12 Combo BM 12 containing b12 heavy and light chains.
                                                                                                                                                                                                                                                                                                           1169
                                                                                                                                                                                                                                                                                                                       1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Figure 29; 374pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                      AAA32151 standard; DNA; 13254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                            832
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AAA3215
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immunoglobulin amino acid sequences from the host cell.
The anti-HIV gp-120 monoclonal antibody is used for providing passive
Immunoglobulin amino acid sequences from the host cell.
The anti-HIV gp-120 monoclonal antibody is used for providing passive
Immunotherapy to HIV in a human. They can be administered to high-risk
patients to reduce the likelihood and/or severity of HIV-induced disease
and to patients who are already HIV-infected. The antibodies are used
for neutralising field isolates which provides information about the
immunocompetence of an immune response in HIV patients, for detecting
HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
producing anti-idiotypic antibodies which can be used for active
immunisation and to screen human monoclonal antibodies to identify those
with the same binding specificity and to monitor the course of HIV disease therapy by measuring the changes in concentration of HIV present
in the body or in body fluids by immunoassay. The anti-HIV gp-120
monoclonal antibodies are encoded by a human polymulectied sequence and
when used in vivo for diagnosis and immunotherapy of HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                      inserting the first and second polynucleotide sequences into a host
                                                           (c) maintaining the host cell in conditions which allow the amino acid sequences encoded by the polynucleotides to be expressed in the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6449 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 6390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6209 TGAGAAAGGCCCACGCTTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with monoclonal antibodies of xenogeneic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6389 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGGTTAACTCGTGTTACCGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGAAAGCGCCACGCTTCCCGAAGGGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012 GTCGGAACAGGAGCGCACGAGGAGCTTCCAGGGGGAAACGCCTGGTATCTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6149 GTCGGAACAGGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13254 BP; 3206 A; 3561 C; 3249 G; 3237 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.9%; Score 454.8; DB 21 99.6%; Pred. No. 1.5e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6029 CGGAGCCTATGGAAAAACGCCAGCAACGCGGCCCGAGG 5992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCGGGGG 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA32165 standard; DNA; 13254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric derivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 456; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                      cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832
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(first entry)

04-JUL-2000

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ctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttg

GACTCAAGACGATAGTTACCGGATAAGGCGCCAGCGGTCGGGCTGAACGGGGGGTTCGTGC

892 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT

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Antibody; anti-HIV monoclonal antibody; glycoprotein-120; human immunodeficiency virus type 1; HIV-1; infectivity titripassive immunotherapy; reduce severity; HIV-induced disease; immunocompetence; active immunisation; ss.
     Complete nucleotide sequence of b12 IgG1 expression vector.
                                                                                                                                                                        Disclosure; Page 291-300; 374pp; English.
                                                                                                                         RA;
                                                                                                                         Lerner
                                                                                                                                                            specific for glycoprotein-120
                                                                                    99AU-0048754.
                                                                                                99AU-0048754
                                                                                                            (SCRI ) SCRIPPS RES INST.
                                                                                                                        Burton DR, Barbas CF,
                                                                                                                                    WPI; 2000-246867/22
                                                                                    16-SEP-1999;
                                                           AU9948754-A
                                                                        17-FEB-2000
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                                                Synthetic.
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TGAGAAAGCGCCACGCTTCCCGAAGGGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGG tgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagg GTCGGAACAGGAGAGCCCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT CCTGTCGGGTTTCGCCACCTCTGACTTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG

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immunoglobulin amino acid sequences from the host cell.

The anti-HIV gp-120 monoclonal antibody is used for providing passive immunotherapy to HIV in a human. They can be administered to high-risk patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the immunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV present in the body or in body fluids by immunoassay. The anti-HIV gp-120 monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for diagnosis and immunotherapy of HIV-induced disease
                                                                                                                                                                                                                                                                                                                                       This sequence represents a polynucleotide used in the preparation of the antibodies of the invention. The invention relates to the production of an anti-law (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity asay by 50% at a concentration of less than 70 mg/ml. The method for the production of the antibody comprises:

(a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAX98206) and a second polynucleotide encoding a light chain immunoglobulin amino acid sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (b) inserting the first and second polynucleotide sequences into a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (c) maintaining the host cell in conditions which allow the amino adsequences encoded by the polynucleotides to be expressed in the host
Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduce the problems of significant host immune response to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric derivation
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This DNA sequence comprises a minimal colE1 origin of replication isolated from vector pVR327 by digestion with BstY1 and AvaI. Novel humanised vectors of the invention (see AAV21724, AAV21727 and AAV21732-34) comprise a human-derived promoter or mammalian homologue which is functional in a mammalian target tissue and cells and an acceptance site which accepts CNA products from RT-PCR cloning. They also contain minimal non-human components that are necessary for production of the vector. The colE1 replication origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anised polynucleotide vectors - comprising human derived promoter sequence acceptance site, used for the production of vaccines % \left( 1\right) =\left\{ 1\right\} =\left\{
ColEl origin of replication from vector pBR327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector; vaccine; ColE1; tumour; antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV21731 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-159552/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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Gaps

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2; Indels

Length 13254;

DB 21;

Score 454.8; DB 21 Pred. No. 1.5e-115; 0; Mismatches

31.9%; 99.6%;

Local Similarity 99.6 nes 456; Conservative

Query Match Matches

Sequence 13254 BP; 3238 A; 3231 C; 3579 G; 3206 T; 0 other;

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TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCGGAACAGGAGGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
                                                                                                                                                                                                                                                                                          provides plasmid replication and growth within permissive strains of Escherichia coli. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                              CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTTTACCGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                         GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
                                                                                                                                                                                                                                                                                                                                   CTGCTAATCCTGTTACCAGTGGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
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                                                                                                                                                                                                                                                                                                                                                 virus; influenza virus; promoter; gene expression; pHL1104; pHL926; ds; cyclic.
                                                                                                                                                                                                                  Score 453.8; DB 19; Length 608; Pred. No. 8.8e-116;
                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                          Sequence 608 BP; 130 A; 175 C; 160 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                  31.8%;
99.6%;
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                                                                                                                                                                                                                                              Matches 455; Conservative
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attenuation;
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other

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CAT cDNA with flanking non-coding sequences from influenza viral RNA segments, inserted in antisense orientation between murine rDNA segments, inserted in antisense orientation between murine rDNA promoter and terminators sequences. The CAT reporter gene replaces a haemagolutinin coding sequencing, retaining viral 5' and 3' cuntranslated sequences, which cooperatively constitute the vRNA untranslated sequences, which cooperatively constitute the vRNA constructs and subsequently with helper influence affected with mutated constructs and subsequently with helper influence affected activity. A double mutant (G3A, UBC) resulted in significant CAT activity, while a triple mutant (G3A, UBC) resulted in viruses with greatly enhanced expression rates. This may be utilized in viral vaccine vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gactcaagacgatagttaccggataaggcgcagcggtcgggctgaacggggggttcgtgc 1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1859 tgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagg 1918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.8%; Score 453.8; DB 17; Length 5241; 99.6%; Pred. No. 2e-115; Live 0; Mismatches 2; Indels 0;
                                                                                                                                       as
                                                                                                                                      - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5241 BP; 1264 A; 1320 C; 1379 G; 1278 T; 0 other;
                                                                                                                                    Attenuated RNA virus with improved expression rate - us vaccine, e.g. against HIV, herpes virus, rhinovirus or cytomegalovirus
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                                                                                                                                                                                                         Disclosure; Page 21-31; 38pp; English.
94EP-0115505
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Best Local Similarity 99.6
Matches 455; Conservative
                                                                                                    WPI; 1996-173036/18
                                                                     Menke A,
                                   (FARB ) BAYER AG.
30-SEP-1994;
                                                                  Hobom G,
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ID AAN906
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AAN90646 standard; DNA; 5365

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                                                                                                                                                                                                                                                                                   Liu TR;
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                                                    pBG394
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    -like polypeptide 9; immunotheraputic; prophylactic; diagnostic.

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                                                 Nucleotide sequence of region encoding first 113 AA of plasmid including soluble T4-like (sT4) polypeptide number 9 (sT4#9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                   DNA sequences coding for soluble T4-like polypeptide(s) - used in immuno:therapeutic and immunosuppressive compsns. and preventing, treating or detecting AIDS
                                                                                                                                                                                                                                                                                   Maraganore JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5365 BP; 1300 A; 1380 C; 1355 G; 1330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.8%; Score 453.8; DB 10; 99.6%; Pred. No. 2e-115; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                   RA,
                                                                                                                                                                                                                                                                                   Flavell
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                                                                                                                                                                                                                                                                                   Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purify HIV from a sample.
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                         (first entry)
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                                                                                       T4-like
                                                                                                                                                                                                                                                                                 Gilbert
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Best Local Similarity
Matches 455; Conserv
                                                                                                                                                                                                                                                         (BIOJ ) BIOGEN INC
                                                                                                   plasmid pBG394;
                                                                                       soluble
                                                                                                                                                                                                                              07-JAN-1988;
                         01-FEB-1991
                                                                                                                                                     WO8901940-A
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                                                                                                                                                                                                                                                                                   Fisher RA,
AAN90645;
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It is the nucleotide sequence of the plasmid pBG395. The sequence was isolated from 2 libraries: a lamda gt cDNA library derived from T cell tumour line REX and a lamda gtl0 cDNA library derived from T peripheral blood lymphicoyes (PBL). For screening, a series of chemically synthesised antisense oligonucleotide DNA probes based on the known T4 protein sequence was used. The polypeptide encoded is useful in immunotherapeutic, prophylactic and diagnostic compsns. It can be used to purify HIV from a sample.
TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; soluble T4-like polypeptide 10; immunotherapeutic; prophylactic; plasmid pBG395; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTAATCCTGTTACCAGTGGCTGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 453.8; DB 10; Length 5413;
Pred. No. 2e-115;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequences coding for soluble T4-like polypeptide(s) - used in immuno:therapeutic and immunosuppressive compsns. and preventing, treating or detecting AIDS
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                                                                              1168
                                                                                                                            3555 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCCGAG 3519
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99.6%;
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Matches 455; Conservative
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                                   1012 GTCGGAACAGGAGGGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT 1071
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Search completed: January 17, 2002, 12:03:06 Job time: 17773 sec

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; MOLECULE TYPE: DNA (genomic)
US-08-276-852-156
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1458.079 Million cell updates/sec
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Sequence 1, Appli
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Appli
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                                                                                                                                                                                                                                                                        1 TGCCATGGCGCGGATTCTT.....CAGCCTCTCCCACAGGTACC 1425
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Sequence 17, A
                                                                                                                             January 17, 2002, 11:52:06; Search time 221.34 Seconds
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-899-575-156
US-08-899-575-156
US-08-899-575-170
PCT-US95-08743-170
US-08-594-469-9
US-08-594-469-1
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US-08-507-455-3
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                                                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1425
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Maximum DB seq length: 200000000
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Sequence 41, Appl
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Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 13, Appli
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Sequence 3, Appli
Sequence 13, Appl
Sequence 13, Appl
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Sequence 13,
Sequence 8, A
                             US-08-447-430A-41

US-08-318-837-10

US-08-333-576C-9

US-08-333-576C-9

US-08-808-324-9

US-07-989-847-13

US-07-989-847-13

US-07-921-848-13

US-07-745-382-13

US-07-745-382-13

US-07-741-372-3

US-08-115-680-3

US-08-115-680-3

US-08-115-680-3

US-08-115-680-3

US-08-115-680-3

US-08-115-680-3

US-08-115-310-3

US-08-115-3

US-08-11
                                                                     331.08
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## ALIGNMENTS

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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIPECATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCR1452P
US-08-276-852-156/c
; Sequence 156, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 619-554-6312
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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FILING DATE: 30-SEP-1992
TORNEY/AGENT INFORMATION:
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                                                                                                                                     772 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
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Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard R
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                      Indels
                       Score 454.8; DB 1;
Pred. No. 9.5e-133;
0; Mismatches 2;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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N: 514
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APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
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                     31.9%;
                                Best Local Similarity 99.6
Matches 456; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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TITLE OF INVENTION: TO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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FILING DATE: 18-JUL
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STATE: CA
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APPLICANT: Burton, Dennis R
APPLICANT: Burton, Carlos Farlos Farl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 454.8; DB 1;
Pred. No. 9.5e-133;
0; Mismatches 2;
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                                                                                                  SCR1452P
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NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCH
TELECOMMUNICATION
TELEPHONE: 619-554-2937
                                                                                                                                                                                            TELEFRUNE: 019-554-6312
INFORMATION FOR SEQ ID NO: 170: SEQUENCE CHARACTERISTICS: LENGTH: 13254 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-276-852-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.9%;
Best Local Similarity 99.6%;
Matches 456; Conservative
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TOPOLOGY: cir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          892 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 454.8; DB 1; Length 13254; Pred. No. 9.5e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6029 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCCGAGG 5992
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                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                       APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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Best Local Similarity 99.6
Matches 456; Conservative
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COMPUTER READABLE FORM:
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                   MEDIUM TYPE:
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6806 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 6865
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                                          GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Burton, Carlos F
APPLICANT: Burton, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 1066 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 454.8; DB 1;
Pred. No. 9.5e-133;
O. Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/899,575
FILLING DATE: 24-JUL-1997
Sequence 170, Application US/08899575 Patent No. 5770440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,163
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99.6%;
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LENGTH: 13254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.9
Best Local Similarity 99.6
Matches 456; Conservative
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1071
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                                                                               1012 GTCGGAACAGGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCCTGGTATCTTATAGT
                                                                                                       1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Larbas, Carlos F
APPLICANT: Larbas, Carlos F
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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CURRENT APPLICATION DATA:
ELLIAND NUMBER: US/08/899,575
FILING DATE: 24-UUL-1997
                                                                                                                                                                                                                                              1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGGGGGG 1169
                                                                                                                                                                                                                                                                    7226 CGGAGCCTATGGAAAACGCCAGCAACGGGGCCGGAGG 7263
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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3R: SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 156, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 156:
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LENGTH: 13254 base pairs
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US-08-899-575-156/c
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6449 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 6390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6089 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTGTGATGATGCTCGTCAGGGGGG 6030
                                                                 712 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
                                                                                                                                                                                    772 CIGCIAATCCIGITACCAGIGGCIGCIGCCAGIGGCGAIAAGICGIGICITACCGGGITG
                                                                                                                                                                                                                                                   832 GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC
                                                                                                                                                                                                                                                                                                                                          ACACAGCCCAGCTTGGAGCGAACGACCTACAGCAACTGAGATACCTACAGCGTGAGCAT
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APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
CITY: La Jolla
CUTY: CA
COUNTRY: USA
ZIP: 92037
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
Pred. No. 9.5e-133;
0: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                            0; Mismatches
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APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UU-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US/08/899,575
24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 170, Application US/08899575 Patent No. 5804440 GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
    99.68;
                         Matches 456; Conservative
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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  Best Local Similarity
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US-08-899-575-170
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Query Match

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MOLECULE TYPE: DNA (genomic)
 INFORMATION FOR SEQ ID NO:
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PCT-US95-08743-170
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                                                                                                                                                                                                                                                                                                                                          Indels
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TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                       Score 454.8; DB 1;
Pred. No. 9.5e-133;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 156, Application PC/TUS9508743 GENERAL INFORMATION:
   ATTONNEL FILLING, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                  ; MOLECULE TYPE: DNA (genomic)
US-08-899-575-170
                                                                                                                                                                                                                                                                                                         31.9%;
99.6%;
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.6
Matches 456; Conservative
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6089 CCTGTCGGGTTTCGCCACCTCTGACTTGACGCGCGATTTTTTGACATGCTCGTCAGGGGG 6030
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TO HUMAN IMMUNOBERICIENCY VIRUS
170
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COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          Score 454.8; DB 5;
Pred. No. 9.5e-133;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6029 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCCGAGG 5992
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INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
                                                                                                                         MOLECULE TYPE: DNA (genomic)
PCT-US95-08743-156
                                                                                                                                                                                                                            31.9%;
99.6%;
                         LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION: TO INUMBER OF SEQUENCES: 17(COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 456; Conserv
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RESULT 10
US-08-906-957-9/C
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STREET: 62
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TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: Periplasmic proteins of prokaryotic microorganisms in the
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                952 TOAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
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                                          Length 13254;
                                                                 Indels
                                     Score 454.8; DB 5;
Pred. No. 9.5e-133;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                              1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGGGGG 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/08594469
; Patent No. 5700665
                                      31.9%;
99.6%;
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                                               Best Local Similarity 99.6
Matches 456; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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PCT-US95-08743-170
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                                    Query Match
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Sequence 9, Application US/08906957
Patent No. 5856142
GENERAL INFORMATION:
APPLICANT: MALDONADO, Paul
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Pred. No. 6.3e-133;
0; Mismatches 2;
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CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                REF/LEGOUX
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET UNMBER: REF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             LENGTH: 1905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%;
99.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.69
Matches 455; Conservative
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periplasmic proteins of prokaryotic microorganisms in the presence of arginine 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                952 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2783 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGCCGGACAGGTATCCGGTAAGCGGCAGG 2724
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                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 453.8; DB 1;
Pred. No. 1e-132;
0; Mismatches 2;
                        extraction
                                                                                                                     ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: VITGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31 - CAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%;
99.6%;
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.6
Matches 455, Conservative
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                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & T
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                              ZIP: 22314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1905;
                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 6.3e-133;
0; Mismatches 2;
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                                                                                                                                                                                                                        FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,469
FILING DATE:
APPLICATION NUMBER: FR 95 01083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08594469
Patent No. 5700665
IBM PC compatible
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APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 455; Conserv
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            2843 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGGGTGAGCAT 2784
                                                                                                                                                                                                               1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
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                                                                            TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PEPINSKY, R. BLAKE
APPLICANT: ROSA, MARGARET D.
APPLICANT: STOSSEL, THOMAS P.
TITLE OF INVENTION: MULTIMERIC GELSOLIN FUSION CONSTRUCTS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02954
FILING DATE: 19910503
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,368
FILING DATE: 04-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 453.8; DB 5;
Pred. No. 1.3e-132;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                           1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGG 1168
                                                                                                                                                                                                                                                                                                                    2603 CGGAGCCTATGGAAAACGCCAGCAACGGGGCCCGAG 2567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application PC/TUS9102954 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 6151 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FISH & NEAVE
STREET: 875 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 455; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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PCT-US91-02954-12
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                                                                                                                                                                                            APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periphasmic proteins of prokaryotic microorganisms in the
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 453.8; DB 2;
Pred. No. 1e-132;
                     2603 CGGAGCCTATGGAAAAGGCCAGCAACACGGGCCCGAG 2567
1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGG 1168
                                                                                                                                                                                                                                                                                                                                                                                     - Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/906,957 FILING DATE: 06-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     Sequence 1, Application US/08906957
Patent No. 5856142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                       STREET: 625 Slaters Lane - CITY: Alexandria
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99.6%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.6
Matches 455, Conservative
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STRANDEDNESS: single
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ADDRESSEE: Bacon & T
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: USA
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772 CIGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTTTACCGGGTTG 831

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TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
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                                                                                                                                                                                                                                                                                                                                         1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG
                                                     GACTCAAGACGATAGTTACCGGATAAGGCGCCAGCGGTCGGGCTGAACGGGGGGTTCGTGC
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TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGGGGG 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/460,343B
FILING DATE: 01-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-mar-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8119 base pairs
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STRANDEDNESS: Single
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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Length 8119;

31.8%; Score 453.8; DB 1;

Query Match

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                                                        712 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
                    Gaps
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TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STRET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                      Indels
    Pred. No. 1.5e-132;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                    0; Mismatches
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APPLICATION NUMBER: US/08/398,028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08398028B; Patent No. 5780285; GENERAL INFORMATION:
99.68;
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 8119 base pairs
  Best Local Similarity 99.6
Matches 455; Conservative
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STRANDEDNESS: Sing
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; TOPOLOGY: Linear
US-08-398-028B-1
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; 0 2642 IGAGAAAGGGCCACGCTTCCCGAAGGGAGAAGGCGGACAGGTATCCGGTAAGCGGCAGG 2583 1012 GTCGGAACAGGAGGGGACGAGGAGGTTCCAGGGGGAAACGCCTGGTATCTTTATAGT 1071 Gaps 952 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG ; 0 Length 8119; Indels Ouery Match
31.8%; Score 453.8; DB 1;
Best Local Similarity 99.6%; Pred. No. 1.5e-132;
Matches 455; Conservative 0; Mismatches 2; q ŏ g δ q δy - Q Qγ q δ Db δ Dp ò

Search completed: January 17, 2002, 11:53:09 Job time: 17316 sec

4A3A-P1H1 4A3A-P8A1 AU081137

nucleic

Run on:

Sequence:

Title:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa; 1 to 615)

2 kang, Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones

1 Homo sapiens CB library cDNA clones

1 Homo sapiens CB library cDNA clones

2 contact: Zhu Chen

3 Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64740490
                                   AU17626 AU176264
AJ281552 4A3A-P6F1
AJ281552 4A3A-P6F1
AL033840 DKF2p434A
AL0339576 DKF2p434B
BF299419 24A-6-11
AL03443 DKF2p434C
BF298419 24A-6-11
AJ28612 AU081124
AJ28613 CAONA int
AJ28619 GAJA-P9E3
BE749047 601123138
BE749147 601123134
BE749147 601123134
BE749147 601123194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lib="CB"
/clone_lib="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoletic stem/progenitor cell"
/lab_host="BM25:8"
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AL042334
AQ876119
AV613078
AQ876011
AG009464
AV604761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. 615
                                     AU176264
AJ281654
AJ281552
AL043846
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KEYWORDS
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AUTHORS
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AL044178 DKFZP434P
AL043613 DKFZP434H
AV735756 AV735756
AJ281661 4A3A-P8G1
BF381364 ASTRO004
AL04364 DKFZP434C
AL593919 AL593919
AJ281480 AA3A-P4G8
AJ281489 AA3A-P4G3
AJ281449 AA3A-P4G3
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2355.323 Million cell updates/sec
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                                                                                                                                ....CAGCCTCTCCCACAGGTACC 1425
                                                                    ; Search time 6501.33 Seconds
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                                                                                                                                                                                                     22703874
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                11351937 segs, 5372889281 residues
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1 TGCCATGGCGCGGATTCTTT....
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Maximum Match 100%
Listing first 45 summaries
                                                                   January 17, 2002, 08:54:03
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Maximum DB seq length: 2000000000
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/note="Vector: pBluescript; Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion"
176 c 159 g 147 t 4 others
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This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ): Email S. Wiemann@UKFZ- heidelberg de;
Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Graman Genome Project.
No rl sequence available.
This clone (DKFZp434G0127) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
Bloecker_H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
                                                                                                                               712 GIGIAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 771
                                                                                                                                               Gaps
                                                                                                                                                                                    772 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG 831
                                                                                                                                                                                                    400 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTCTTACCGGGTTG 341
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                                                                                           Length 615;
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On Jul 8, 1999 this sequence version replaced gi:5866785.
Contact: Bloecker H
                                                                                                                  4; Indels
                                                                                        DB 10;
                                                                               31.6%; Score 450.2; DB 10;
99.1%; Pred. No. 2.7e-116;
iive 0; Mismatches 4;
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                                                                                                       452; Conservative
                                                                                          Local Similarity
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                                                                             Query Match
                     BASE COUNT
ORIGIN
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AL043585/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 571)
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                                                                                                                                                                                                                                                               Length 527;
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Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5866789.
Contact: Bloecker H
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                           2; Indels
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                                                                              /clone_lib="434 (synonym: htes3)"
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/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: Not:3 a 158 c 137 g 119 t
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                                                                                                                                                                                                                                                 31.6%; Score 449.8; DB 10
99.6%; Pred. No. 3.3e-116;
tive 0; Mismatches 2;
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                                    1. .527
/organism="Homo sapiens"
/db_xref="taxon:9606"
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DKFZp434P0828_s1 434 (synonym: ht
DKFZp434P0828 3', mRNA sequence.
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                                                                                                                                                                                                                                                                             451; Conservative
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and

Berlin. 6, 14059

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This is the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the CDNA sequencing consortium of th
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                       Brandt, P., Mewes, H.W., Gassenhuber, J.
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AV735756 CB Homo sapiens CDNA clone CBMAGCO3 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                              No r1 sequence available.

This clone (DKFZp434H1527) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
1. .579
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Pred. No. 3.4e-116;
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/tissue_type="testis"
/dev_stage="adult"
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This is the 3' sequence of the clone inse
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                     Bloecker, H., Boecher, M.,
                                                               EST (Bloecker, et al.)
Unpublished (1999)
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99.6%;
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                                                                                                              Contact: Bloecker H
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                       AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         German Genome Project.

No rl sequence available.
This clone (DKFZp434P0828) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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                                       Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de, sequenced by GBF (National Research Centre for Biotechnology Braunschweig/Germany) within the cDNA sequencing consortium o
                                                                                                                                                                                                                                                                                                                                                                                                                            Vector: pSport1; Site_1: Not1; Site_2: Sall"
c    149 q    132 t
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                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="Dkr2p434P0828"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/lab_host="Ph108"
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Pred. No. 3.4e-116;
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DKFZp434H1527 3', mRNA sequence.
ALO43613
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Query Match

Matches

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403 ( 832 892 283 952

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AL043613/c

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                                                                                                   Lang, O., Ye, W., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z., Chen, S., Mao, M. and Chen, Z. and Chen, S., Mao, M. and Chen, Z. and Chen, S., Mao, M. and Chen, Z., Unpublished (2000)

Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
17 Rui-Jin II Road, Shanghai 200025, P. R. China
Fax: 86-21-64740306
                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pBluescript; Site_1: EcoR1; The insert is cloned randomly with the EcoR1 digestion"
182 c 165 g 143 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
Shanghai.
                                                                                                                                                                                                                                                                 Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 449.8; DB 10; Length 616; 99.6%; Pred. No. 3.5e-116; Live 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAGC03"
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AV735756.1 GI:10853337
                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CB"
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/colone_lib="Anopheles gambiae immune competent 4A3A"
/coll_line="immune competent 4A3A"
/lab_host="b. coli DHI0B"
/note="Vector: p7730-Pec (Pharmacia) with a modified
polylinker; Site_l: EcoRi, Site_2: Not!; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
(1996): Normalization and Subtraction: Two approaches To
Racilitate Gene Discovery, Genome Research 6, 791-806."
                                                                                                                                                                         Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                            Anopheles.

[ (bases 1 to 617)
Dimpoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
                                                                                                                                                                                                                                                                                                                                Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
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                                      AJ281661 617 bp mRNA EST 30-JUN-2000
4A3A-P8G10-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P8G10, mRNA sequence.
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Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heldelberg, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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99.6%; Pred. No. 3.5e-116;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P8G10"
                                                                                                                                                        African malaria mosquito.
                                                                                                 AJ281661
AJ281661.1 GI:6929540
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Matches 451; Conservative
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952 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
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Unpublished (1999)
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The differentially expressing genes pool from Anopheles stephensi related to infection with Plasmodium yoelii enriched by suppression subtractive hybridization
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mosquito Genes Pool Related Malaria Infection"
/sex="female"
/tissue_type="whole body"
                                                                                                                                                                                    ASIRO004 Mosquito Genes Pool Related Malaria Infection Anopheles stephensi cDNA 5', mRNA sequence.
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Contact: Xu Xiaochun; Qu Fengyi; Song Guanhong; Xu Jiannong
                                                          128 CCTGTCGGGTTTCGCCACCTCTGACCTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGG
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178 c 169 q 136 t
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Pred. No. 3.5e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Parasitology
Second Military Medical University
Boo Xiangyin Rd., Shanghai, 200433, China
Tel: 86 021 25070276
Email: xcxu@smmu.edu.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Anopheles stephensi"/strain="Hor"
                                                                                                   1132 CGGAGCCTATGGAAAACGCCAGCAACGCGGCC 1164
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                                                                                                                    quality sequence stop: 629
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1 (bases 1 to 628)
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POLYA=No.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemanndekfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp434C172) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

1. .954
                                                                                                                                                                              1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
                                                                                                                                                                                                      209 CCTGTCGGGTTTCGCCCACCTCTGACCTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 150
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329 TGAGAAAGCGCCACGCTTCCCGAAGGGAAAAGGGCGGACAGGTATCCGGTAAGCGCAGG
                                                                         1012 GTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                    269 GTCGGAACAGGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCCTGGTATTTTATAGT
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Pred. No. 4e-116;
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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273 c 253 q 21
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DKFZp434C172_s1 434 (synonym: h
DKFZp434C172 3', mRNA sequence.
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/lab_host="DH108"
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No rl sequence available.
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AL593919 XGC-gastrula Silurana tropicalis cDNA clone TGas003010 5',
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I (bases 1 to 629)

Huckle, E., Taylor, R., McMurray, A., Ashurst, J.L., Zorn, A.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/dboxref="taxon:8364"
/clone="tracas003010"
/clone=lib="xcc-gastrula"
/dev_stage="gastrula"
/dev_sta
                                                                                                                                                                                                     TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
                                                                                                                                                                                                                                                                                                          GTCGGAACAGGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGF 1071
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                                                                                                                            832 GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC 891
                                                                           672
                                                                                                                                                                                                                              Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropésanger.ac. uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_1D: TGas003010.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
                        892 ACACAGCCCAGCTIGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
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larity 99.6%; Pred. No. 6.7e-116;
Conservative 0; Mismatches 2; I
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Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1132 CGGAGCCTATGGAAAAACGCCAGCAACGCGGCC 1164
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
                     952 TGAGAAAGCGCCACGCTTCCCGAAGGGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011
                                                                                                                                                                                                                                                                                                                                                                                                    1012 GTCGGAACAGGAGGGGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTATAGT 1071
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GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
                                                                           CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTTTACCGGGTTG
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                                                                                                                                                                                892 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT
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/cell_line="immune competent 4A3A"
/lab_nost="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                              1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
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European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, C
Location/Qualifiers
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/clone="4A3A-P4G8"
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Anopheles gambiae
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; Anopheles.
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oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
1 262 c 244 g 244 t 2 others
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) 20300950
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                                                                                                                                                                                                                                                                                                415 CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG 356
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                                                                                                                                                                                                             GACTCAAGACGATAGTTACCGGATAAGGCGCCGCGCGGGCTGAACGGGGGGTTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 448.8; DB 10; Length 1004; 99.3%; Pred. No. 7.8e-116; Live 0; Mismatches 3; Indels 0;
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Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg,
Location/Qualifiers
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1 (bases 1 to 703)
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                                                                                                                                          Similarity
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/db_xref="taxon:7165"
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polylinker; Site=1: EcoRI; Site=2: NotI; sequenced from
polylinker; Asite=1: EcoRI; Site=2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea
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Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   712 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
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Pred. No. 1e-115;
0; Mismatches 3;
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99.3%;
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1 (bases 1 to 800)
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nes 450; Conserv
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Query Match
31.4%; Score 447.8; DB 10
Best Local Similarity 99.1%; Pred. No. 1.2e-115;
Matches 449; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                              /organism="Anopheles gambiae"
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                                     African malaria mosquito.
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                    KEYWORDS
SOURCE
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MEDLINE
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/clone_11bner: site_11 EcoRI; Site_2: Not!; sequenced from polylinker; Site_1: EcoRI; Site_2: Not!; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA ilbrary that was constructed from the 4A3A call line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares Facilitate Gene Discovery, Genome Research 6, 791-806."
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                                                   Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
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Best Local Similarity
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ORIGIN
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I (bases 1 to 568)
Dimopoulos, Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) ó TGAGAAAGCGCCACGCTTCCCGAAGGGAAAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1011 712 GIGIAGCCGIAGIIAGGCCACCACTICAAGAACICIGIAGCACCGCCIACAIACCICGCI 771 772 CIGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG 831 1012 GTCGGAACAGGAGGGCGACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTATAGT 1071 347 1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131 Gaps 891 287 892 ACACAGCCCAGCTIGGAGGGAACGACCTACACGAACTGAGATACCTAACAGCGTGAGCAT 951 167 ; 0 DB 10; Length 568; 4; Indels Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany. 1132 CGGAGCCTATGGAAAAACGCCAGCAACGCGGCC 1164 δ

37

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cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
57 a 196 c 189 g 146 t 2 others
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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1 (bases 1 to 700)
Inchapoulos, C., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donobue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B.
and Kafatos, F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) 20300950
                                                   1012 GTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT 1071
                                                                                                                                                    1072 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ281616 700 bp mRNA EST 30-JUN-2000 4A3A-P8A12-F Anopheles gambiáe immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P8A12, mRNA sequence.
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216 TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 157
                                                                                                                                                                               712 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
                                                                              Length 700;
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99.1%; Pred. No. 1.3e-115;
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European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, C
                                                                                                                                                                                                                                                      /strain="4A r/r"
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forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.
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Meyerhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
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/organism~"Anopheles gambiae"
46 CGGAGCCTATGGAAAAACGCCNNCAACGCGGCC 14
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                                                                                                                                                    579 bp
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synthetic construct.
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Erickson,S. and Schwall,R.
Methods of treatment using anti-erbb antibody-maytansinoid
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Sequence 1 from Patent W00100244.
AX060703.
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Result
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                                                                      January 17, 2002, 11:49:01; Search time 10436.3 Seconds (without alignments) 3359.081 Million cell updates/sec
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1 GCCACCATGGCCCTGACCT.....AGCCTCTCCCACAGGTACCT 2125
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                           1472140 seqs, 8248589755 residues
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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121129 159750 RNNEUR HAMNEU AX027785 AR038307 AR038321

4062 11795 13254 13254 13254 13254 6649

I21124 I59745 HUMHER2A

A49702 XXU13846 SYNPBR329

A52326 AR027062 I86195

477043

X99274 Artificial AX003206 Sequence AR002333 Sequence AR018032 Sequence

ASPNGV

22-JAN-2001

PAT

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Parter: WO 0100244-A 1 04-JAN-2001; Genentech, Inc. (US) Location/Qualifiers source FEATURES

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DEFINITION
ACCESSION
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                                            Length 9274;
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                                            Score 672; DB 6; 1
Pred. No. 3.6e-156;
0; Mismatches 45;
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AR080259
 or sequence"
2489 q 20
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  /note="vector
                                           Query Match 31.6%;
Best Local Similarity 93.9%;
Matches 710; Conservative (
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Unclassified.
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                                                                                                                                                     Length 4473;
           Antisense oligonucleotide modulation of human HER-2 Patent: US 5968748-A 1 19-OCT-1999;
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Bennett, C. Frank, Lipton, A. and Witters, L.M.
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                                                                         /organism="unknown"
1383 c 1329 g
                                           Location/Qualifiers
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X03363
X03363.1 GI:31197
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Best Local Similarity
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2353. .3132
/note="aa 727-986, seq. homologous to EGF receptor kinase
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Pred. No. 6e-156;
0; Mismatches 33;
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                                 2446. .2454
/note="pot. glycosylation s
4455. .4460
/note="put. polyA signal"
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DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4473)
                                                                                                                                                                                                                                                                                                              The c-erb-B-2 protein shows similarity to the epidermal growth factor receptor.
cell surface glycoprotein; cellular oncogene; erB-2 cellular; glycoprotein; growth factor receptor; kinase; neu cellular oncogene; transmembrane protein; tyrosine kinase.
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                                                                                                                 Yamamoto,T., Irana,S., Akiyama,T., Semba,K., Nomura,N., Miyajima,N., Saito,T. and Toyoshima,K. Similarity of protein encoded by the human c-erb-B-2 genepidermal growth factor receptor Nature 319 (6050), 230-234 (1986)
                                                                                                                                                                                                                               Papewalis,J., Nikitin,A.Yu. and Rajewsky,M.F.
G to A polymorphism at amino acid codon 655 of the human
erbb-Z/HER2 gene
Nucleic Acids Res. 19 (19), 5452 (1991)
92020265
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175. .3442
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/product="put. c-erb-B-2 protein (aa 1-1234)"
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949. .957
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/note="c-erb-B-2 precursor"
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/note="pot. glycosylation
2059. 2067
/note="pot. glycosylation
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/strain="cell line MKN-7"
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/note="pot. 9
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5518885

Sequence 9 from patent US

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Pred. No. 1.5e-155;
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                                                      1 (bases 1 to 4530)
Razluddin,. and Sarkar,F.H.
ERBE2 promoter binding protein in n
Patent: US 5518885-A 9 21-MAY-1996,
                                                                                          Location/Qualiflers
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/organism="unknown"
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95.2%;
          GI:1601478
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95.2%; Pred. No. 1.5e-155;
tive 0; Mismatches 34;
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Razluddin; and Sarkar, F. Hoque.
Antibody to ERBB2 promoter binding
Patent: US 5654406-A 9 05-AUG-1997;
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LMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFREL
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FCPDPARGGGAVHHRHRSSFRRSGGODLTLGLEDSEEERAFSPLASESGGSSDYFDG
DLGMGAAKGLOSLPFTHDSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNOPDVR
PQPPSPREGPLDPARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAA
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4530; 1 to 4530; 1 to 4530; 1 to 4530; Coussens, L., Yang-Feng, T.L., Liao, Y.-C., Chen, E., Gray, A., Kordzath, J., Seeburg, P. H., Libermann, T. A., Schlessinger, J., Francke, U., Levinson, A. and Ullrich, A.
3885 CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAACCAGAAGGCCAAGTCCGCAGAAGCC 3944
                                                                                                                               Human tyrosine kinase-type receptor (HER2) mRNA, complete cds M11730
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                                                                                                                                                                                   Homo sapiens (clone: lambda-HER2-436) fetal cDNA to mRNA.
Homo sapiens
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Science 230 (4730), 1132-1139 (1985)
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Pred. No. 1.5e-155;
0; Mismatches 34;
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/db_xref="taxon:9606"
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/note="HER2 receptor"
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Ullrich, A.
Unpublished (1988)
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95.2%;
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Chromosome 17q21-q22.
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Matches 701; Conservative
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Cheever,M.A. and Disis,M.L.
Methods for eliciting or enhancing reactivity to HER-2/neu protein
Patent: US 586945-A I 09-FEB-1999;
Location/Qualifiers
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3345 CTCTGAAGAGGGCCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGCCTGGCTCCGATGT 3404
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Sequence 1 from patent US 5869445.
AR034479
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Catarrhini; Hominidae; Homo.
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                                                                                      TCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCA 3674
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                                     228 ACGCCAGCAGAAGATCACATGTCCAGACCCTGCCCGGGCGCGTGGGGGCATGGTCCACCA 287
                   Gaps
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Methods of treatment using anti-erbb antibody-maytansinoid
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Length 3768;
                   Indels
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Score 667.6; DB 6;
Pred. No. 4.8e-155;
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                   0; Mismatches
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Sequence 2 from Patent WO0100244.
AX060704
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Location/Qualifiers
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31.4%;
98.6%;
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         Similarity 98.6
14; Conservative
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                   Matches 684;
Query Match
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Canis familiaris cDNA to mRNA.

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 3780)

Yokota, H.
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                                                                                                             Score 666; DB 6;
Pred. No. 1.2e-154;
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Canis familiaris mRNA for erbB-2,
AB008451
1. .3768
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 1170 c 1121 g 71
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ilarity 98.4%;
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Patent: WO 0148205-A 1 05-JUL-2001;
CORIXA CORPORATION (US)
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Sequence 1 from Patent WO0148205.
AX189662
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1105 c 1068 g
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MirrivgcGovvgorlelytlpanssisflodiotyggyvllargovrgiplorspu
RGTQLFEDNYALAVLDNGDPLEGGTPAPGAAGGLRELQLRSLTEILKGGVLIQRSPQ
RGTQLFEDNYALAVLDNGDPLEGGTPAPGAAGGCRELQLRSLTEILKGGVLIQRSPQ
LCHQDTILWROVFHKNNGDLALTLIDTNRFSACPPCSPACKDAHGWGASSGDCGSLTRT
VCAGGCARCKGPOPTDCCHEDCAAGCTGPKHSDCLACHFNNSGICELHCPALVTYNT
DTFESMPDFGRAYTGAACYTSCPYNLSTDYGSCTLUCPLNOSTYAEDGTQRCEKC
SKPCARVCYGLGMEHLREVARAVTSANYQEFAACKKIFGSLAFLDESFEGGDPASWTAPL
OPRQLRYFGALGLIHRNARAVTSANYQEFAACKKIFGSLAFLDRANPELLGGG
SMLGLRSLRELGSGLALIHRNARALCVYTYVBWDQLFRNPQALLHSANRPEECCYGG
CAPCARGWGPGPTQCVKCSQFLRGQGCVECRVLQGLPRRYVCRSCLDCHSGC
CQPOMGSVTCFGSBADQCVKCSQFLRGQGCVECRVLQGLPRRYVCHSGLGGG
CAPCARGWGPGPTQCVKCSQFLRGQGCVECRVLGGLPRRYVKLGSGAFGTVQF
CPINCTHSCADLDEKGCPARQRSYPYSILAAVVGLLLGILLKRRQKIR
KYTRRRLQFTBLARGRLGSGOLLUMCVQIAGKGSPYVGGLGGILSTYVQLYTQ
LMPYGCLLDHVREHRGRLGSGOLLUMCVQIAGKGSPYVGTLGILTSTVQLYTQ
LMPYGCLLDHVREHRGRLGSGOLLUMCVQIAGKGSPYVGTLGILTSTVQLYTQ
WTFGGARLLDDTBTFRERDLDRGKYPYRKELLY
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QPPLALEGPLPPSRPAGATLERPKTLSPKTLSPGKNGVVKDVFAFGSAVENPEYLAPR
GRAAPQPHPPPAFSPAFDNLYYWDQDPSERGSPPSTFEGTPTAENPEYLGLDVPV"
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CPEPTPGAGGTAHRRHRSSSTRNGGGELTLGLEPSEEEPPKSPLAPSEGAGSDVFDGD
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               Submitted (23-OCT-1997) to the DDBJ/EMBL/GenBank databases. Hiroshi Yokofa, Rakuno Gakuen University, Veterinary Biochemistry; Bunkyoudaimidorimati, Ebetsu, Hokkaido 069, Japan (E-mail:BXA03503@niftyserve.or.jp, Tel:011-386-1111,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGCCACCACCACCACCACCACCACCAGAATGCCGTGGTGAGCTGACTCTAGGACTGGAGCC 3191
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                                                                                                                               cDNA cloning of erbB-2 from canine mammary gland Published Only in DataBase (1997) In press Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 516.2; DB 4;
Pred. No. 1.8e-117;
0; Mismatches 88;
                                                                                                                                                                                                    /organism="Canis familiaris"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                    /product="erbB-2"
/protein_id="BAA23127.1"
/db_xref="G1:2575867"
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2 (bases 1 to 3780)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                   GGGAGGAGCTGCCCCTCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGCCTTCGACCTT
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Pred. No. 1.2e-115;
0; Mismatches 127;
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1 (bases 1 to 3955)
Raziuddin, .. and Sarkar,F.H.
BRBE2 promoter binding protein in ne-
Patent: US 5518885-A 14 21-MAY-1996;
Location/Qualifiers
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                 712 TTTGGGGGTGCCGTGGAGAACCCCG-AGACTTGACACCCCAGGGAGGAGGTGCCCCTCAG
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472 AGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGC
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Pred. No. 2.1e-112;
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Raziuddin,. and Sarkar,F. Hoque.
Antibody to ERBE2 promoter binding fe
Patent: US 5654406-A 14 05-AUG-1997;
Location/Qualifiers
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US 5654406,
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159750.1 GI:2478382
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83.0%;
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Lofts,F.J., Hurst,H.C., Sternberg,M.J. and Gullick,W.J.
Specific short transmembrane sequences can inhibit transformation
by the mutant neu growth factor receptor in vitro and in vivo
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                               3290 GATGGTGACCTGGCAATGGGGGTAACCAAAGGGCTGCAGAGCCTCTCTCCACATGACCTC 3349
                                                                                                     CTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGACGTTTTTGCC 711
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                                                                                      CCCCAGCCCCCTTCGCCCCGAGAGGGCCCTCTGCCTGCTGCCGGACCTGCTGGTGCCACT
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The neu oncogene encodes an epidermal growth factor
receptor related protein
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/db_xref="taxon:10116"
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/protein_id="CAA27059.1"
/db_xref="G1:56746"
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Oncogene 8 (10), 2813-2820 (1993)
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RFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLLEDDDMGDLVDAEEYLV PQQGFFSPDPTPGTGSTAHRRHRSSSTRSGGGELTLGLEPSEEGPPRSPLAPSEGAGS DVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAPLACSPQPEYVN QSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLVP 1; LTGTICTSGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALV GNPQLCYQDMVLWKDVFRKNNQLAPVDIDTNRSRACPPCAPACKDNHCWGESPEDCQI REGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAENPEYLGLDVPV" 3110 CAGCAGGGATTCTTCTCCCCGGACCCTACCCCAGGCACTGGGACACACGCCCATAGAAGG 3169 292 CACCGCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTCT 351 Gaps 232 CAGCAGAAGATCACATGTCCAGACCCTGCCCCGGGCGCTGGGGGCATGGTCCACCACAG AGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGC Length 3955; DB 10; phosphorylation site" phosphorylation site" phosphorylation site" 23.3%; Score 495.8; DB 10; 83.0%; Pred. No. 2.1e-112; iive 0; Mismatches 117; phosphorylation site' /product="put. p185 (aa 1-1241)" /note="pot. glycosylation site" glycosylation site" glycosylation site" phosphorylation 1136 q 830 t /note="pot. p 3723. .3725 /note="pot. p a 1147 c 1 pot. 2662 "pot. /note="pot. 1916. 1924 /note="pot. 3695. .3697 /note="pot. 2087. .2089 .235 74. .3796 Matches 577; Conservative /note="p 2660. .2 /note="p 3446. .3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura,T.
Direct Submission
Submitted (19-MAY-1993) to the DDBJ/EMBL/GenBank databases. Takuro
Nakamura, Faculty of Medicine, University of Tokyo, Department of
Pathology; 7-3-1 Hongo, Bunkyo-ku, Tokyo-113, Japan
(Tel:03-3812-2111(ex.3356), Fax:03-3815-8379)
Takuro Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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Nakamura,T., Ushijima,T., Ishizaka,Y., Nagao,M., Arai,M.,
Yamazaki,Y. and Ishikawa,T.
Cloning and activation of the Syrian hamster neu proto-oncogene
                                                                                                                                                                                                                                                                              831 CCACCAGAGGGGGGGGTCCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCA 890
                                                                                                          TTTGGGGGTGCCGTGGAGAACCCCG-AGACTTGACACCCCAGGGAGGAGGTGCCCCTCAG
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/isolate="animal 14"
/db.xref="taxon:10036"
/cell_line="14-2"
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Faculty of Medicine, University of Tokyo
                                                                                                                                                                                                                                                                                                                                                   891 GAGTACCTGGGTCTGGACGTGCCAGTGTGAAGCCT 925
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03-3815-8379.
Location/Qualifiers
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Mesocricetus auratus
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Bunkyo-ku Tokyo 113
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PQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGGAVENPEYLVPRGGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGGTGACCTGGGAATGGGGGGAGCCAAGGGGGTGCAAAGCCTCCCCACACATGACCC
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/cell_type="neoplastic Schwann cell"
/clone_lib="NHH3T3"
/tlssue_type="peripherall nerve"
33. .3797
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1209 c 1182 g 826
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/protein_id="BAA03801.1"
/db_xref="G1:747595"
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33. .3797
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Bollen,A., Jacobs,P., Jacquet,A., Haumont,M. and Massaer,M.G.
Varicella-zoster virus vaccines
Varicella-zoster virus vaccines
SMITHKLINE BEECHAM BIOLOG (BE) : BOLLEN ALEX (BE) ; JACOBS PAUL
(BE) ; JACQUET ALAIN (BE) ; HAUMONT MICHELE (BE) ; MASSAER MARC
GEORGES FRANCIS (BE)
Location/Qualifiers
3649 AACCCCATCCTCCCCCCCTTGTGCCCACCTTTGACAACCTCTATTACTGGGACCAGGACC 3708
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                                                                                                                                                                                                                                                                                          832 CACCAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAG
                                     CCCCAGCCCCCTTCGCCCCGAGAGGGCCCTCTGCCTGCTGCCGGACCTGCTGGTGCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.4%; Score 454.8; DB 6; Length 11795;
99.6%; Pred. No. 2.8e-102;
tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
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/db_xref="taxon:32630"
1 2760 c 2957 g 3161 t
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                                                                                                                                                                                                                                                                                                                                                                                                                        AX027785 11795 bp DNA
Sequence 4 from Patent WO0043527.
AX027785
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1591 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT 1650
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                                                                                                                                                                                                                                                 567
                                                                                                                                       626 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
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Fri Jan 18 08:27:38 2002

Human HER-2/neu pr Human heregulin 2 Mouse Her-2/neu CD

Human HER-2∕neu on

Human HER-2/neu co Rat neu promoter. Rat HER-2/neu prot Human breast and o

Nucleotide sequenc

Perfect score:

Title:

Sequence:

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Scoring table:

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Minimum DB Maximum DB

Database

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//trag= b
//note="combined splice and polyA sequences"
1195.1401
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/note= "ColE1 origin of replication"
1877..2125
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/product= human HER-2/neu
922..1181
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/note= "RANTES promoter"
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AAA59345
AAT40915
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AAN90647
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AAT50962
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AAN90645
AAN90644
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AAT01590
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AAT27307
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13..921
/*tag= a
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/note= "SupF gene"
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Chimeric - Escherichia coli.
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                                                                             misc_feature
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HER-2 nucleic acid
HER2 transgene pla
Her-2/neu (ERBB2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HER2 gene.
Nucleotide sequenc
CDNA encoding the
HER-2/neu oncogene
                                                                                                                                (without alignments)
3037.069 Million cell updates/sec
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Humanised vector p
Humanised vector p
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                                                                                                                                                                                           2125
1 GCCACCATGGCCCCTGACCT......AGCCTCTCCCCACAGGTACCT 2125
                                                                                                             ; Search time 599.86 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **Since State Stat
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            930621 seqs, 428662619 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           January 17, 2002, 12:03:06
                                                                               - nucleic search, using sw model
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AAV21724
AAV21726
AAO46083
AAE24297
AAF1253
AAT71253
AAT10585
AAT40139
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Score

Result Š.

Plasmid pBG381 inc Sol.rhesus CD4 seq Plasmid pinf 4-49.

Full length T4

Full length T4 cDN Plasmid p170-2 inc Subtilisin N62D/G1

Complete sequence

us-09-242-202a-22.rng

540

CAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCC

481

2

Fri

WO9806863-A1

19-FEB-1998

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Plasmid pITL-hHER2/neu comprises base vector pITL (see AAV21724) and a human HER2/neu nucleic sequence. pITL-hHER2/neu was used to evaluate the toxicity of anti-tumour vaccination in rats, and in phase I and phase II trials to evaluate polynucleotide vaccination in advanced breast cancer. Novel humanised vectors, which can be based on pITL, comprise a human-darived promoter or mammalian homologue which is functional in mammalian target tissue and cells
                                                                                                                                                                                                                                                          comprising human derived promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells but are capable of extended stable expression of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence, generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other component
                                                                                                                                                                                                                                                                              the production of vaccines
                                                                                                                                                SERVICES
                                                                                                                                                                                                                                                                          and sequence acceptance site, used for
                                                                                                                                                                                                                                                                                                              Example 7; Page 41-42; 125pp; English.
                                                                                                                                                                                                                                                          Humanised polynucleotide vectors
                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN
                                                                       97WO-US14306
                                                                                                            96US-0023931
                                                                                                                                                                                     Nelson PJ
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                                                                     14-AUG-1997;
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other; T; 0 G; 428 C; 598 Sequence 2125 BP; 449 A; 650

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1440 1020 1020 1080 1260 agtggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataaggcg 1560 1261 agggagcaggccagtaaaagcattacccgtggtggggttcccgagcggccaaagggagca 1320 1561 CAGCGGTCGGCTGAACGGGGGGTTCGTGCACACACCCCAGCTTGGAGCGAACGACCTAC 1620 840 960 540 900 009 099 099 720 720 780 780 840 900 006 661 cccaagactctctccccagggaagaatggggtcgtcaaagacgtttttgcctttgggggt GCCGTGGAGAACCCCGAGACTTGACACCCCAGGGAGGAGCTGCCCCTCAGCCCCACCTC 721 geogragagaacecegagaettgacaceceagggaggaggagctgeeeeteageeeeeeee GGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTGG GTCTGGACGTGCCAGTGTGAAGCCTTAAGGGCCATATGGTGAGTGGATGCCTTGACCCCA GGCGGGGATGGGGGAGACCTGTAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCC 1021 TTCCCCTGCAGTGAGTAGTGACTGCCCGGGTGGGATCCCTGTGAGCCCTCCCCAGTGCCT 1081 ctcctggccctggaagttgccactccagtgcccaccagccttgtcctaataaaattaagt TGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTATAAGCTTGATATCGAATTCTT 1141 tgcatcattttgtctgactaggtgtcctctataaatattataagcttgatatcgaattctt 1201 TCTCAACGTAACACTTTACAGCGCGCGCGTCATTTGATATGATGCGCCCCGCTTCCCGATA AGGGAGCAGCCAGTAAAAGCATTACCCGTGGTGGGGGTTCCCGAGCGGCCAAAGGGAGCA TTCAAAAGTCCGAAAGAATTCCTGCAGCCCGTGTAGCCGTAGTTAGGCCACCACTTCAAG AGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG CCTTCGCCCCGAGGGCCCTCTGCCTGCTGCCGACCTGCTGGTGCCACTCTGGAAAGG 781 CTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCAGGACCACAGAGC 841 ggggggctccacccagcaccttcaaagggacacctacggcagaaacccagagtacctgg 901 gtctggacgtgccagtgtgaagccttaagggccatatggtgagtggatgccttgacccca CTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGT 1441 AACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCC 481 cagcggtacagtgaggaccccacagtacccctgccctctgagactgatggctacgttgcc 1141 541 ( 961 1201 1261 1321 1381 901 1081 601 721 841 1381 1501 199 g qq Db g Óλ Dp δŽ g δŏ g ÓΥ q δy g δ g ò ð Op δŽ δ g QΥ g Óγ g QY g δ g δ 셤 δ δy g δ δ

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                                             AAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTT 1740
                                                                      CCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAG 1800
                                                                                               CGTCGATTTTTGTGATGCTCGTCAGGGGGGGGGGGCCTATGGAAAAACGCCAGCAACGCG 1860
                                                                                                                         GAATTICCGGAGCTATITCAGITTTCTTTTCCGTTTTGTGCAATTTCACTTATGATACCG 1980
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                   ACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGA
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/*tag= b
/note= "combined splice and polyA sequences"
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/note= "ColEl origin of
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Chimeric - Escherichia coli
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polynucleotide vectors. Such vector for novel humanised
polynucleotide vectors. Such vectors comprise a human-derived
promoter or mammalian homologue which is functional in mammalian
target tissue and cells and a sequence acceptance site (see
AAV21735-36), which accepts CDNA products from RT-PCR cloning. They
also contain minimal non-human components, such as a replication
or righn (see AAV21715) and selectable marker gene (see AAV21717-18) that
are necessary for production of the vector, as well as human-derived
corigin (see AAV21715). The novel vectors are
used to express target antigens, especially tumour antigens.
they
are non-replicating in mammalian cells but are capable of extended
stable expression of target sequences generating an immune response
to inmunised individuals. The vectors selectively elicit immune
responses to the target sequences with little or no immune response
to the other components of the vectors. The target antigens are
content of a sintracellular polypeptides or peptides and, as such,
are processed as self polypeptides or peptides and appropriately
presented on antigen presenting cells.
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                                                                                                                                                                                                                                                                                                                                                                          Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
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100.0%; Pred. No. 2.9e-299;
ive 0; Mismatches 0;
                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 29-30; 125pp; English.
                                                             97WO-US14306
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Matches 1203; Conservative
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14-AUG-1997;
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                                                  polyA_site
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Synthetic
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                                          <u> AGCGGCAGGGTCGGAACAGGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTAT</u>
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                                                                                                                                             tumour; antigen; plasmid pITLGFP;
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- Escherichia coli.
- Aequorea victoria.
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plasmid pITL-GFP comprises base vector pITL (see AAV21724) and a humanised green fluorescent protein (GFP) reporter sequence can humanised dreen fluorescent protein (GFP) reporter sequence can mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which carcepts cDNA products from RT-PGF cloning. PITL-GFP was used to examine the kinetics of expression of a reporter sequence from such vectors in an animal model (Fisher 344 rats). Toxicity from such vectors in an animal model (Fisher 344 rats). Toxicity from such vectors in an animal model (Fisher 344 rats). Toxicity from such vectors target antiqens, especially tumour antiques. They are non-replicating in mammalian cells but are capable of extended is target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
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                                                                                                                                                             /*tag= b
/note= "combined splice and polyA sequences"
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                                                                                                                                                                                                                                                                                                                                                                                             "ColE1 origin of replication"
                                                                                         /product= green fluorescent protein 720..967
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Pred. No. 5.3e-297;
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location/Qualifiers
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Best Local Similarity 99.9
Matches 1195; Conservative
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                          TGCCCACCAGCCTTGTCCTAATAAATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCT
                                            tgcccaccagccttgtcctaataaaattaagttgcatcattttgtctgactaggtgtcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGGCTGCAAAGCCTCCCACACATGA
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                                                                                                                                        c-erbB-2; glycoprotein;
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 CDNA; 4299
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P-PSDB; AAR39568.
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Matches 702; Conserv
AAQ46083 standard;
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                                    AAQ46083,
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                                                                                                                                                                                                                                                                                                           HER-2; c-neu; ErbB2; transmembrane receptor; tyrosine kinase activity; epidermal growth factor receptor; EGFR; HER-1; cancer; breast cancer; ovarian cancer; gastric cancer; antisense oligonucleotide; expression; hyperproliferative disease; ss.
                                      707
                                                                                                                                                            treat hyperproliferative conditions,
                                                  3495 cactctggaaaggcccaagactctctccccagggaagaatggggtcgtcaaagacgtttt
                                                                  TGCCTTTGGGGGTGCCGTGGAGAACCCCGAG - ACTTGACACCCCAGGGAGGAGCTGCCCC
                                                                                                                               GGACCCACCAGGGGGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAAA
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     CACTCTGGAAAGGCCCCAAGACTCTCCCCCAGGGAAGAATGGGGGTCGTCAAAGACGTTTT
                                                                           Examples; Page 38-39; 44pp; English.
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STATE RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bennett CF,
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This is the human HER-2 polynucleotide sequence. The HER-2 gene also called crneu and ErbB2, encodes a transmembrane receptor, with tyrosine kinase activity. HER-2 is related to the epidermal growth factor receptor (EGFR or HER-1). Aberrant HER-2 expression is present in a wide number of cancers, especially breast, ovarian and gastric cancers. This sequence is used in the invention to design 12-25 nucleotide

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oligonucleotides that decrease the expression of human HER-2. The oligonucleotides of the invention (AAZ31067-Z31070) can also be used for modulating the expression of human epidermal growth factor receptor. The oligonucleotides are used to treat diseases or conditions associated with HER-2, particularly hyperproliferative diseases ann as associated with
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                                                                                                               Sequence 4473 BP; 902 A; 1383 C; 1329 G; 859 T; 0 other;
                                                                                                                                                              31.6%; Score 671.2; DB 20;
ilarity 95.4%; Pred. No. 1.8e-162;
Conservative 0; Mismatches 33;
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CACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGGTCGTCAAAGACGTTTT
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                                                                                                                                                                                                                                                                                                               Treating tumors, particularly breast cancers, which overexpress an ErbB receptor and does not respond to an anti-ErbB antibody, comprises conjugating the antibody to a maytansinoid -
                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                     cancer;
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                                 Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9274 BP; 2152 A; 2539 C; 2488 G; 2095 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.5%; Score 670.4; DB 22;
93.8%; Pred. No. 3.7e-162;
Live 0; Mismatches 46;
           HER2 transgene plasmid construct,
                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 4; 92pp; English.
                                                                                                                                                            23-JUN-2000; 2000WO-US17229
                                                                                                                                                                                    25-JUN-1999; 99US-0141316.
16-MAR-2000; 2000US-0189844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 93.8 tes 709; Conservative
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                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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                                                                                                          WO200100244-A2.
                                                                      Homo sapiens.
Synthetic.
                                                antibody; ds
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                                                                                                                                                                                                                                                     CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAAGCCTTAAGGGCCCATATGGTGAGTGG
                                                                 TCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCA
                                                                                                                                    GGACCCACCAGAGCGGGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified protein binding to the ERBB2 gene promoter - to i cell proliferation, diagnostic of breast cancer, also related antibodies, nucleic acid, assays and methods for screening
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cellular immunogen; cancer; self-determinant immunoreactivity; cancer vaccination; breast carcinoma; colon carcinoma; immunotherapy;

proto-oncogene; ss

Homo sapiens

cognate transgene; human; tyrosine kinase-type

Human

us-09-242-202a-22.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 669.6; DB 16; Length 4530;
Pred. No. 4.5e-162;
0; Mismatches 34; Indels 1;
    a decreased chance of long-term survival. Binding of HPBF to promoter can be inhibited using antisense ollgonucleotides or non-genomic nucleic acid that binds to HPBF; these ollgos can expressed from retro virus or other gene therapy vectors.
                                               Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;
decreased chance of long-term survival.
                                                                                31.5%;
95.2%;
                                                                                                Matches 701; Conservative
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                                                                                        Best Local Similarity
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BP.

AAT71253 standard; DNA; 4530

AAT71253 RESULT

(first entry)

30-MAR-1998

AAT71253;

C X C X E X

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This sequence represents the human HBR2 cognate transgene (CTG).
Deletion of amino acids 1-731 of the encoded protein renders the CTG
non-transforming. HBR2 is a tyrosine kinase-type receptor. This sequence can be used in the cellular immunogen of the invention. The cellular immunogen of the invention is for immunishing against the product of a target proto-oncogene, over-expression of which is associated with a cancer, comprises host cells transfected with a construct containing at promoter. The product of the transgene induces immunoracityity to host promoter. The product of the transgene induces immunoracityity to host self-determinants on the product of proto-oncogene. The cellular immunogens are used for protective vaccination against cancer (e.g. carcinoma of breast or colon, or various lymphomas) and for immunotherapy of cancer. Use of the immunogen liminates the need to isolate immunogenic, HLA host-matched peptides. The method is not based on immune reconstruction.
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                                                                                                                                                                                                                                                                                                         Proto-oncogene immunogen - used in vaccine for the prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 ACGCCAGCAGAAGAICACATGTCCAGACCCTGCCCGGGCGCTGGGGGCATGGTCCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 669.6; DB 18; Length 4530; 95.2%; Pred. No. 4.5e-162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            generates a systemic (anti-metastatic) response.
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                                                                                                                                                                           97WO-US00582.
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                                                                                                                                                                                                                                                                                                                          treatment of cancer
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                                                                                                                     WO9725860-A1
                                                                                                                                                                                                   9-JAN-1996;
                                                                                                                                                                                                                                                      England JM,
                                                                                                                                                24-JUL-1997
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product of a target proto-oncogene which is associated with a malignanacy. The cellular immunogen comprises allogenic cells transfected with transgene construct comprising a transgene cognate to target proto-oncogene and a strong promoter. The cellular immunogen is useful for vaccinating a host against cancer by inserting the transgene construct into the body of the host for the expression of the transgene. The method of the invention is designed to target mutation-driven non-self determinants. The cellular immunogens induce reactivity for self-determinants in the over expressed product of tumour associated and over expressed proto-oncogenes.
                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumourigenic; cellular immunogen; immunisation;
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                                                                                                                                                                     TGCCTTTGGGGGTGCCGTGGAGAACCCCGAG-ACTTGACACCCCAGGGAGGAGGTGCCCC
                                                                                                                                                                                                                                                                     tgcctttggggggtgccgtggagaaccccgagtacttgacaccccagggaggagctgcccc
                                                                                                                                                                                                                                                                                                          TCAGCCCCACCCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCA
                                                                                                                                                                                                                                                                                                                             GGACCCACCAGAGCGGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAA
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                                                              proto-oncogene; malignanacy; allogenic cell; vaccine; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a cognate transgene of c-neu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 66-68; 77pp; English.
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ENGLAND J M.
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                                                                                                                                                     ACGGCAGCAGAAGATCACATGTCCAGACCCTGCCCCGGGCGCTGGGGGCCATGGTCCACCA 287
                                                                                                          Gaps
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                                                                                                                                                                              31.5%; Score 669.6; DB 21; Length 4530; 95.2%; Pred. No: 4.5e-162;
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                                                                                                          Indels
Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;
                                                                                                          34;
                                                                                                          0; Mismatches
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                                                                                                          Matches 701; Conservative
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                                                                                      Similarity
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3549 iggctacgitgccccctgacctgcagcccccagcctgaatatgigaaccagccagatgt 3608
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                                                                           468 CCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGA
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/mote= "nucleotides 2026-3765 (claim 1) code for
HER-2/neu intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase;
breast cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; genetic immunisation; tumour; vaccine; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           887 CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAAGC 923
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1..3765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US01689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disis ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-455361/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HER-2/neu oncogene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The conserved cysteine residues, compared to the unspliced protein. The crbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of treating cancer. Substances which stimulate SPLICE erbB-2 are useful for reducing tumor cell proliferation and for treating conditions involving damaged cells including conditions. Involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
                                                                                                                SPLICE erbB-2 receptor protein; cell transformation disorder; cancer; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3249 acccagcagggettettetgtecagaceetgeecegggegetggggggggtgggeegea 3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ACGGCAGCAGAAGATCACATGTCCAGACCCTGCCCCGGGCGCTGGGGGGCATGGTCCACCA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
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                                                                                    cDNA encoding the SPLICE erbB-2 receptor protein.
                                                                                                                                                                                                                                                             /*tag= a
/product= "SPLICE erbB-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.5%; Score 669; DB 21;
98.4%; Pred. No. 6.5e-162;
tive 0; Mismatches 10;
                                                                                                                                                                                                                                  Location/Qualifiers
175..3942
standard; cDNA; 4472
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                                                          (first entry)
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Best Local Similarity 98.45
Matches 686; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muller WJ, Siegel PM;
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P-PSDB; AAY84780.
                                                                                                                                                                 wound healing; ss.
                                                                                                                                                                                                                                                                                                     WO200020579-A1.
                                                     08-AUG-2000
                                                                                                                                                                                              Homo sapiens
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3735 cccagagtacctgggtctggacgtgccagtgtga 3768
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                                                                                                                          c-erbB2) protein (AAMOIII). The oncogene is overexpressed in various cancers, including breast, ovarian, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or deregulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the CDNA sequence code for the intracellular domain (Lys676-Vall255) of the HER-2/neu protein, which is useful for immunisation against malignancy.

Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral vector, for genetic immunisation of an animal.
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                                                                                                               Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or
                                                                                                                                                                                                                                                                                                                                                                                             ACGGCAGCAGAGATCACATGTCCAGACCCTGCCCGGGCGCTGGGGGCGTTGGTCCACCA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACCCACCAGGGGGGGGGCTCCAGCCAGCACTTCAAAGGGACACCTACGGCAGAGAA
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                         DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is
                                                                                                                                                                                                                                                                                                                                     DB 17; Length 3768;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                       Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                  31.4%; Score 667.6; DB 1'98.6%; Pred. No. 1.4e-161 'ative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGA 920
                                                                                Claim 1; Page 49-56; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                  Similarity
P-PSDB; AAW01111
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Matches 684;
                                                       associated
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This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailgnancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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                                                                                                                                                                                     oncogene; immune response; T cell; B cell; immunisation;
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for treating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "region which elicits immune response"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of HER-2/neu polypeptides - for eliciting an an HER-2/neu associated malignancy, particularly preventing tumours
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                                                                                                                                                                                                                                                                                                                                                                         /product= "HER-2/neu"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..3768
                                                                                                                                                                                                                                                                                                                                                                                          /note= "oncogene"
2026..3765
/*tag= b
                                                                                                                                                                                                              malignancy; treatment; tumour; ss.
                                                                                                                                       Human HER-2/neu oncogene DNA.
AAX01912 standard; DNA; 3768
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93US-0033644.
93US-0106112.
95US-0414417.
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Best Local S
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                          408 ATTIGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGTGCAAAGCCTCCCCACACATGA
                                                                                TGCCTTTGGGGGTGCCGTGGAGAACCCCGAG-ACTTGACACCCCAGGGAGGAGGAGCTGCCC
                                                                                                                                                                                                  GGACCCACCAGGGGGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAA
                                                           Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2; ds.
                                                                                                                                                                                                                                                        /product= "HER-2/neu protein"
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                                                                                                                                                                                                                                                                                                                                      Human HER-2/neu protein encoding DNA
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1..3768
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Hand-Zimmermann

Cheever MA,

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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents a DNA encoding the human HER-2/neu protein (also known as pl85 or c-erbb2).
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                                                                  enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
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                                                    New antigen-presenting cells, useful as vaccines for eliciting
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                          P-PSDB; AAB85458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine kinase; cytostatic; vaccine;
                                                                                                                                                                                                                         breast cancer; prostate cancer; ovarian cancer; lung cancer; colon cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.3%; Score 666; DB 21;
98.4%; Pred. No. 3.6e-161;
tive 0; Mismatches 10;
3735 cccagagtacctgggtctggacgtgccagtgtga 3768
                                                                                                                                                 Human heregulin 2 (Her2) coding sequence.
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                                                                   AAA09455 standard; DNA; 3768
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P-PSDB; AAY92620.
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The present sequence encodes the mouse Her-2/neu protein. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The Her-2/neu gene is an oncogene. An Her-2/neu fusion protein comprising a domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the Her-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
for vaccinating against breast, ovarian, colon, lung and
                                                            Disclosure; Fig 19; 128pp; English
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Sequence 3771 BP; 808 A; 1105 C; 1068 G; 790 T; 0 other; 23.9%; 82.3%; Query Match 23.9 Best Local Similarity 82.3 Matches 596; Conservative

DB 21; Length 3771;

1; 198 GGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCACATGTCCAGACCC 257 258 TGCCCGGGGGCTGGGGGCATGGTCCACCACGCACCGCAGCTCATCTACCAGGAGTGG 317 CGGTGGGGACCTGACATAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCCAGGTCTCCACT 377 GGCACCCTCCGAAGGGGCTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGGGGAGC 437 CAAGGGGCTGCAAAAGCCTCCCCACACATGACCCCAGCCCTCTACAGGGGTACAGTGAGGA 497 1; Gaps Score 508.8; DB 21; Length Pred. No. 8.5e-121; 0; Mismatches 127; Indels 318 378 438 οy ŏ ρp QQ δŏ δλ qq Qγ qq οy Ω

3527 677 737 AGACTIGACACCCCAGGGAGGAGCTGCCCCTCAGCCCCACCTTCCTGCTTCAGCCC 796 CCCTCTGCCTGCTGCCGACCTGCTGCTGCCACTCTGGAAAGGCCCAAAGACTCTCTCCCC 857 CACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGT 618 Q δ ò

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Search completed: January 17, 2002, 12:03:53 Job time: 17820 sec

GTGA 920

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Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 3, Appli Sequence 40, Appl Sequence 10, Appl Sequence 10, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli

Sequence

Sequence Sequence

Run on:

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Sequence 1, Application US/09048804
Patent No. 5968748
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STARE: PA
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MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: IBM FC compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%; Score 671.2; DB 2;
llarity 95.4%; Pred. No. 7.4e-175;
Conservative 0; Mismatches 33;
                                        US-07-415-307A-1
US-08-371-320-1
US-08-09-038-141-1
US-08-507-455-4
US-08-447-430A-42
US-08-447-430A-41
US-08-318-837-10
US-08-318-837-10
US-08-333-576C-9
US-08-808-324-9
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US-07-989-847-13
US-08-469-411-13
US-07-745-382-13
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CLASSIFICATION
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUBBER: 38,534
REFERENCE/DOCKET NUBBER: 151S-2913
TELECHONE: (215) 568-3100
TELEPHONE: (215) 568-319
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4473 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
Unknown
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Best Local Similarity
Matches 702; Conserv
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US-09-048-804-1
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Sequence 9, Appli
Sequence 1, Appli
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Sequence 15, Appl
Sequence 156, App
Sequence 170, Appli
Sequence 9, Appli
Sequence 1, Appli
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1 GCCACCATGGCCCTGACCT.....AGCCTCTCCCACAGGTACCT 2125
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2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-35-786-1
US-08-229-515A-14
US-08-276-852-14
US-08-276-852-170
US-08-899-575-170
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Listing first 45 summaries
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Result Š. 1,

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Pred. No. 7.4e-175;

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APPLICANT: KIPPS, THOMAS J.
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REPERENCE: 233/21
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT PILING DATE: 1998-04-06
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASESEQ for Windows Version 3.0
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Patent No. 6287569
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ORGANISM: Homo sapiens
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Length 4473;

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Score 671:2;

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Query Match

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APPLICANT: SARKAR, FAZJUL H
TITLE OF INVENTION: BRBBZ PROMOTER BINDING PROTEIN
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: NEEDLE & ROSENBERG PC: 127 Peachtree Street, Suite 1200 Atlanta
            0; Mismatches
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Best Local Similarity 95.4
Matches 702; Conservative
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STATE: Geor
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GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FALUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/645,865 FILING DATE: 14 MAY 1996
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95.2%; Pred. No. 2.1e-174;
tive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  Sequence 9, Application US/08645865 Patent No. 5654406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414
TELEPHONE: 404-688-9770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4530 base pairs
                                                                                                         3945 CTGATGTGTCCTCAGG 3960
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Best Local Similarity 95.2
Matches 701; Conservative
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STRANDEDNESS: single
                                                                       947 ATGCCTTGACCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
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                                                                                                                                                                  RESULT 4
US-08-645-865-9
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                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 669.6; DB 1;
Pred. No. 2.1e-174;
0; Mismatches 34;
                                                                                            FILING DATE: 19 APR 1994
CLASSIFICATION: 435
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%;
95.2%;
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Matches 701; Conservative
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COMPUTER READABLE FORM:
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US-08-229-515A-9
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3885 CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAACCCAGAAGGCCAAAGTCCGCAGAAGCC 3944
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
                                                                                                          3465 CCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGA 3524
                                             3705 TGCCTTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGACACCCCAGGGAGGAGCTGCCCC 3764
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                                                                                        5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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REGISTATION UNDHER: 32,629
REFERENCE/DOCKET UNDHER: 920010.448C7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08625101
Patent No. 5869445
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TELEFAX: (206) 682-6031
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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OUTHER OF SEQUENCES:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle STATE: Washing
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US-08-625-101-1
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                                                                                                                                        Length 3768;
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APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
                                                                                                                                                                         Indels
                                                                                                                                       Score 667.6; DB 2;
pred. No. 6.7e-174;
0; Mismatches 9;
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                                                                                                                                       31.4%;
98.6%;
                                                                                                                                                                       Conservative
TYPE: nucleic acid
                             TOPOLOGY: linear FEATURE:
                                                                                                                                                       Similarity
                                                             CDS
             STRANDEDNESS
                                                            NAME/KEY:
                                                                          ; LOCATION:
US-08-625-101-1
                                                                                                                                                                      684;
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                                                                                                                                       Query Match
Best Local S:
Matches 684
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3110 CAGCAGGATTCTTCTCCCCGGACCCTACCCCCAGGCACTGGGAGCACAGGCCTAGAAGG 3169
                     3495 CACTCTGGAAAGGCCCAAGACTCTCCCCAGGGAAGAAGAAGAGGGGTGTCAAAGACGCTTT 3554
                                                                                              708 TGCCTTTGGGGGTGCCGTGGAGAACCCCGAG-ACTTGACACCCCAGGGAGGAGCTGCCCC 766
                                                                                                                                                    TCAGCCCCACCTTCTGCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCA 826
                                                                                                                                                                                                                               GGACCCACCAGGGGGGGGGCTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAA 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 495.8; DB 1;
Pred. No. 1.2e-126;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                          3735 CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGA 3768
                                                                                                                                                                                                                                                                                                      CCCAGAGTACCTGGGTCTGGACGTGCCAGTGTGA 920
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Suite 1200
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FILING DATE: 19 APR 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33.438
REFERENCE/DOCKET NUMBER: 1114.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08229515A Patent No. 5518885 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NEEDLE & ROSENBERG STREET: 127 Peachtree Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.3
Best Local Similarity 83.0
Matches 577; Conservative
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STATE: Georgia
COUNTRY: usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-08-229-515A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3315 CCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGA 3374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGA 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3768;
                                   Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "product = "cerB-b2""
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 667.6; DB 2;
Pred. No. 6.7e-174;
0; Mismatches 9;
                                                 Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/356,78
                                                                                                                                                                                                                                                                                                                                                                                                                                        CRP-053
                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                            07/831,967
                                                                                                                                                                    E: Floppy disk
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98.6%;
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Best Local Similarity 98.69
Matches 684; Conservative
                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
                                                                                          STATE: Massachusetts
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 1..3768
; OTHER INFORMATION:
US-08-356-786-1
NUMBER OF SEQUENCES:
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                                                                         Boston
                                                                                                              USA
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                                                                                                                              02109
                                   ADDRESSEE:
                                                                                                              COUNTRY:
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3170 CACCGCAGCTCGTCCACCAGGAGGGGGGGGGGGGGCTGACACTGGGCCTGGAGCCTCG 3229
                                                                           TITGGGGGTGCCGTGGAGAACCCCG-AGACTTGACACCCCAGGGAGGAGCTGCCCTCAG 770
                    412 GATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAAGCCTCCCCACACATGACCCC
                                                                                                      472 AGCCCTCTACAGGGGTACAGTGAGGACCCCACAGTACCCCTGCGCCTGTGAGACTGATGGC
                                                                                                                                                                                         592 CCCCAGCCCCTTCGCCCCGAGAGGGCCCTCTGCTGCTGCTGCTGCTGGTGCTGCTACT
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APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
                                                                                                                                                                                                                                                                                                                                                                                                                3770 GAGTACCTAGGCCTGGATGTACCTGTATGAGACGT 3804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,438
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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352 GAAGAGGAGGCCCCCAGGȚCTCCACTGGCACCCTCCGAAGGGGCTGGCTCCGATGTAITT 411
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Pred. No. 1.2e-126;
0; Mismatches 117;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 404-688-0770
                         TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                            23.3%;
83.0%;
                                                                                                                                                                                                                       Matches 577; Conservative
                                                                                                                              linear
                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                           ; TOPOLOGY:
US-08-645-865-14
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6089 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG 6030
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                                                                                                                                                                                                                                                                                                       APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 1066 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 454.8; DB 1;
Pred. No. 4e-115;
                                                                                            6029 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCCGAGG
                                                                      1831 CGGAGCCTATGGAAAAACGCCAGCAACGCGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-1994
ON: 514
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                                                                                                                                                                                                                                Sequence 170, Application US/08276852 Patent No. 5652138
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
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99.6%;
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 456; Conserv
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
                                                                                                                ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite
STREET: Mail Drop TPC8
                                                                                            ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18 JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/954,148 FILING DATE: 30-SEP-1992 ATTORNEY AGENT INFORMATION:
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APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
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TYPE: nucleic acid
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                                           NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Matches 456; Conserv
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                                                                                                                                                                                  CITY: La Jolla
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                                                1591 ACACAGCCCAGCTTGGAGCGAACGACCTACAGCGAACTGAGATACCTACAGCGTGAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute, Office of ADDRESSE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  1831 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGGG 1868
                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
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FILING DATE: 18-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 156, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lerner, Richard A TITLE OF INVENTION: HUMAN NEI TITLE OF INVENTION: TO HUMAN
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nucleic acid
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MEDIUM TYPE: Floppy
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US-08-899-575-156/c
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                                                                                                                            Length 13254;
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HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla
                                                                                                                                                                 Indels
                                                                                                                   Score 454.8; DB 1;
Pred. No. 4e-115;
0; Mismatches 2;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
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Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZI
TITLE OF INVENTION: TO HUMAN IMMUNOD
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ivvoLoGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-899-575-156
                                                                                                                     21.48;
99.68;
                                                                                                               Query Match
Best Local Similarity 99.6
Matches 456; Conservative
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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US-08-899-575-170
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1411 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 1470
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                                 Suite 220
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Pred. No. 4e-115;
0; Mismatches 2; Indels
   ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road,
STREET: Mail Drop TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY,AGENT INFORMATION:
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                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 156: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.4%; 99.6%; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 456; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                         STREET: Mai
CITY: La JC
STATE: CA
COUNTRY: US
                                                                                                                                                                        92037
ADDRESSEE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
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                           08/178,302
                                                                                                                  US 07/954,148
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Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
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US-08-899-575-170
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99.6%;
FILLING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08
FILLING DATE: 30-SEP-1993
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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Matches 456;
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STRANDEDNESS:
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TITLE OF INVENTION: HUMAN NEUFRALIZING MONOCLONAL ANTIBODIES
TITLE OF TOWNENTION: TO HUMAN IMMUNOBETICIENCY VIRUS
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                          ADDRESSEE: The Scripps Research Institute, Office of ADDRESSE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 STREET: La Jolla STATE: CA
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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99.6%; Pred. No. 4e-115;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/276,852
FILING DATE: 18-JUL-1994
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
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24-JUL-1997
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                                                                                                               Sequence 170, Application US/08899575 Patent No. 5804440 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 170:
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US-08-899-575-170
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.69
Matches 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 9203/
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       circular
                                                                                                                                                         APPLICANT: Burton,
APPLICANT: Barbas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                RESULT 14
US-08-899-575-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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6926 GACTCAAGACGATAGTTACCGGATAAGGCGGAGCGGTCGGGCTGAACGGGGGGTTCGTGC 6985
                                          1591 ACACAGCCCAGCTIGGAGCGAACGACCTACAGCTGAGATACCTACAGCGIGAGCAT 1650
                                                                                                                            TGAGAAAGCGCCACGCTTCCCGGAAGGGAGAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1710
                                                                                                                                                  1411 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1591 ACACAGCCCAGCTTGGAGCGAACGACCTACACGGAACTGAGATACCTACAGGGTGAGCAT 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1651 TGAGAAAGGGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1710
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                                                                1711 GTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
                                                                                                                                                                                                                                  1771 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: BATENTIN Release #1.0, Version #1.25 (EP-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-UUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UUL-1994
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             1831 CGGAGCCTATGGAAAACGCCAGCAACGCGGCCGGGGG 1868
                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 21.4%; Score 454.8; DB 5; Best Local Similarity 99.6%; Pred. No. 4e-115; Matches 456; Conservative 0; Mismatches 2;
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TruS95-08743-156/c
Sequence 156, Application PC/TUS9508743
GENERAL INFORMATION:
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Search completed: January 17, 2002, 11:54:39 Job time: 17406 sec

<sup>6089</sup> CCTGTCGGGTTTCGCCACCTCTGACTTGACGTCGATTTTTGTGATGCTCGTCAGGGGG 6030 1771 CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1830

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Ciona int 4A3A-P9E3 601123138

Homo sapi 601123315

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DKFZp4340

V133£1 mT AV613078 V132B5 mT

AV613078 AQ876011 AG009464 I

DKFZp434A DKFZp434D

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AU176264

DKFZp434E

4A3A-P4D5 4A3A-P2G2 4A3A-P1H1 4A3A-P8A1 AU081137

uq93b02.y 4A3A-P4C3

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Run on:

Sequence:

Searched:

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Half human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

(Y., Sugano,S., Isogai,T.)

(Dnpublished (2000)

Contact: Takao Isogai

Genomics Laboratory
Helix Research Institute
1532-3 Yana , Kisarzau, Chiba 292-0812, Japan
Tel: 81-438-52-3951

Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota'T., Wakamatsu,Â., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU123871 685 bp mRNA EST 23-OCT-2000
AU123871 NT2RM2 Homo sapiens CDNA clone NT2RM2001211 5', mRNA
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/organism="Homo sapiens"
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AJ281616
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Location/Qualifiers
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AU123871.1 GI:10948587
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Mammalia; Eutheria; P
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COMMENT
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AU123871
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KEYWORDS
SOURCE
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  LOCUS
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BG283493 602407782
BII54872 602902857
AA496412 zv37a02 r
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AL043585 DKFZp4349
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AV735756 AV735756
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1 GCCACCATGGCCCTGACCT.....AGCCTCTCCCACAGGTACCT 2125
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                          11351937 seqs, 5372889281 residues
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Maximum Match 100%
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                     228 ACGGCAGCAGAAGATCACATGTCCAGACCCTGCCCCGGGCGCTGGGGGCATGGTCCACCA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIH-MGC http://mgcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG283493 621 bp mRNA EST 21-FEB-2001
602407782F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4519652
                                               NT2
                                                                                                                                                                                                                 ATTTGATGGTGACCTGGGAATGGGGGCCAGCCAAGGGGCCTGCAAAGCCTCCCCACATGA
                                                                                                                                                                                                                                                                                                                                           468 CCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTCTGAGACTGA
                                                                                                                                                                                                                                                                                                                                                                                      588 TCGGCCCCAGCCCCTTCGCCCCGAGGGCCCTCTGCCTGCTGCCGACCTGGTGC
                                                                                                                                         4;
                                          /note="Vector: pME18SFL3; mRNA from uninduced precursor cells" 3 orbers
                                                                                                                  685;
                                                                                                                   Length
                                                                      others
                                                                                                             Score 507.2; DB 10; Length
Pred. No. 3.5e-116;
0; Mismatches 21; Indels
                                                                     3
         /clone_lib="NT2RM2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
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                                                                    123
/clone="NT2RM2001211"
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                                                                 198 g
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                                                                                                               23.9%;
95.6%;
                                                                                                           Query Match 23.9
Best Local Similarity 95.6
Matches 542; Conservative
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BG283493
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/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tab_host="adenocarcinoma, cell line"
/t
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
http://mage.lnl.gov
High quality sequence stop: 602.
Location/Qualifiers
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Pred. No. 7.8e-110;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4519652"
DCTD/DTP
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97.0%;
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Matches 522; Conservative
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/sex="Female"
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                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                        1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: egapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GGAGCTGGTGCTGAAGAGTACCTGGTACCCCAGCAGGGATTCTTCTCCCCAGACCC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 CAAGGGCTGCAAAGCCTCCCCACACATGACCCCAGGCCCTCTACAGCGGTACAGTGAGGA 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 TCCCACATTACCTCTGCCCCCGAGACTGATGGCTACGTTGCTCCCTGGCCTGCAGCCC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 CCAGCCTGAATATGTGAACCAGCCAGATGTTCGGCCCCAGCCCCCTTCGCCCCGAGAGGG 617
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                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lighten distribution in MCC. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1090 row. b column: 15
High quality sequence stop: 764.
Liocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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Pred. No. 3.7e-109;
0; Mismatches 128; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5032238"
BI154872.1 GI:14614873
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Best Local Similarity 81.8%;
Matches 589; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                 1. .791
                                       house mouse
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 649)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality, sequence stop: 257.
                                                                                                                                                                                                              795
                                                                                                                                                                                                                                                                  856 GCACCTTCAAAGGGACACCTACGGCAGAACCCAGAGTACCTGGGTCTGGACGTGCCAG 915
                                                                                                 548 TGGGAAAAATGGGGTTGTCAAAGACG-TTTTGCCTTTGGGGGTGCTGTGGAGACCCTGA 606
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Zv37A02.11 Soares ovary tumor NBHOT Homo sapiens "DNA clone
IMAGE.755786 5' similar to gb:M1130 ERBB-2 RECEPTOR
PROTEIN-TYROSINE KINASE PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                         AGACTTGACACCCCAGGGAGGTGCCCCTCAG-CCCCACCCTCCTCCTGCCTTCAGCC
AGGGAAGAATGGGGTCGTCAAAGACGTTTTTGCCTTTTGGGGGTGCCGTGGAGAACCCCG-
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Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:75786"
/clone_lib="Soares ovary tumor NbHOT"
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Gaps

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459

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/note="Vector: pBluescript, Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion" 176 c 159 g 147 t 4 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              1..615
/organism="Homo sapiens"
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/tissue_type="cord blood"
/cell_type="Cord blood"
/cell_type="Cord blood"
/cell_type="Cord blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 ACACAGCCCAGCTTGGAGCGAACGAACTACACCGAACTGAGAGTACCTACAGCGTGAGCTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA EST 29-FEB-2000 (Synonym: htes3) Homo sapiens cDNA clone
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Unpublished (1999)
On Jul 8, 1999 this sequence version replaced gi:5866785.
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                          Length 615;
                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                    21.2%; Score 450.2; DB 10; 99.1%; Pred. No. 6.2e-102;
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DKFZp434G0127_s1 434 (synonym: h
DKFZp434G0127 3', mRNA sequence.
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AL043585.3 GI:5935889
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Lases 1 to 615)

Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,

Chen, S., Mao, M. and Chen, Z.

Homo sapiens CB library cDNA clones

Unpublished (2000)

Sontact: Zhu Chen

Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Faz: 86-21-64740499

Fax: 86-21-6474030
                             S.
                                                    339 GCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGGTGG 398
                                                                                                                         399 CTCCGATGTATTGATGGTGACCTGGGAATGGGGGCAGCCAAGGGGCTGCAAAGCCTCCC 458
                                                                                                                                                                                              CACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCCCACAGTACCCCTGCCCTC 518
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AV735664 CB Homo sapiens cDNA clone CBNAME07 5', mRNA sequence.
                                                                        755 AGGAGCIGCCCCTCAGCCCCCCCCCCCTCCTGCCTTCAGCCCTTCGACAACCTCTA 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mbshiems.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
                           ..
6
                           Indels
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Chinese National Human Genome Center at Shanghai
Best Local Similarity 87.3%; Pred. No. 3.2e-103; Matches 557; Conservative 0; Mismatches 72;
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RESULT 5 AV735664/C LOCUS DEFINITION

ORGANISM

KEYWORDS SOURCE

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

ACCESSION VERSION

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                            Wiemann, S
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            This is the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Bmail s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                 Berlin.
6, 14059
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                                                                                              No II sequence available.

This clone (DKFZp434G0127) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg (Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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119 t
                                                                                                                                                                                                                                                                                                                                                                Length 527;
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Am Klopferspitz 18a D-82152 Martinsried, Germany
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/organism="Homo sapiens"
/db_are="taxon:9606"
/clone="DKRZp43460127"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                               Score 449.8; DB 10
Pred. No. 7.5e-102;
0; Mismatches 2;
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158 c 137 g 11
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Matches 451; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin.
6, 14059
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                            Brandt, P., Mewes, H.W., Gassenhuber, J.
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                                                                                                                                   sequence version replaced gi:5866789
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No rl sequence available.

This clone (DKFZp434P0828) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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Pred. No. 7.7e-102;
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This is the 3' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p434P0828"
/clone_lib="434 (synonym: htes3)"
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168 c 149 g 1:
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/dev_stage="adult"
/lab_host="DH10B"
                            Bloecker, H., Boecher, M.,
                                                                           EST (Bloecker, et al.)
Unpublished (1999)
On Jul 9, 1999 this sec
Contact: Bloecker H
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Best Local Similarity 99.6%;
Matches 451; Conservative
(bases 1 to 571
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                                                                                                                                                                             Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                  No rI sequence available.
This clone (DKEZp434H1527) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKE2p434H1527"
/clone_lib="434 (synonym: htes3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.2%; Score 449.8; DB 10
99.6%; Pred. No. 7.7e-102;
tive 0; Mismatches 2;
AL043613 579 bp mRNA
DKFZp434H1527_s1 434 (synonym: ht
DKFZp434H1527 3', mRNA sequence.
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/lab_host="DH10B"
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EST (Bloecker, et al.)
Unpublished (1999)
Contact: Bloecker H
MIPS
                                                                 AL043613.1 GI:5423000
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                                                                                                                 Homo sapiens
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                                                                                                    human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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L (bases I to 616)
L (chen, 2. Mao, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z., Chen, S., Mao, M. and Chen, Z.
Chen, S., Mao, M. and Chen, Z.
Unpublished (2000)
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
                                                                                                                                                       AV735756 616 bp mRNA EST 17-OCT-2000
AV735756 CB Homo sapiens cDNA clone CBMAGC03 5', mRNA sequence.
AV735756
AV735756.1 GI:10853337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 21.2%; Score 449.8; DB 10; Length 616; Best Local Similarity 99.6%; Pred. No. 7.8e-102; Matches 451; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript; Site_1: EcoRI; cloned randomly with the EcoRI digestion" 182 c 165 g 143 t l others
1831 CGGAGCCTATGGAAAACGCCAGCAACGCGGCC 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAGC03"
                       57 CGGAGCCTATGGAAAAACGCCAGCAACGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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1 (bases 1 to 628)
Xu,X., Qu,F., Song,G. and Xu,J.
The differentially expressing genes pool from Anopheles stephensi related to infection with Plasmodium yoelii enriched by suppression Gubtractive hybridization
Unpublished (2001)
Contact: Xu Xiaochun; Qu Fengyi; Song Guanhong: Xu Jiannong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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/clone_lib="Mosquito Genes Pool Related Malaria Infection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF381364 628 bp mRNA EST 27-NOV-2000 ASIR0004 Mosquito Genes Pool Related Malaria Infection Anopheles stephensi cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                           CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 1830
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                         1591 ACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCAT 1650
                                                                                                               TGAGAAAGCGCCACGCTTCCCGAAGGGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG 1710
                                                                                                                                                                                                   GTCGGAACAGGAGGGCGCCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT 1770
                                                569 GIGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGGT 510
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/dev_stage="24 hours post-infection"
178 c 169 g 136 t
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Pred. No. 7.9e-102;
0; Mismatches 2;
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Matches 451; Conservative
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/clone_inp="Anopheles gambiae immune competent 4A3A"
/call_line="immune competent 4A3A"
/lab_host="E. coli DHIOB"
/note="Vector: p7730-Pac (Pharmacia) with a modified
colva. The 4A3A is a directionally cloned and normalized
colva. The 4A3A is a directionally cloned and normalized
colva. The 4A3A is a directionally cloned and normalized
colva. The factor of the factor of the
/normalization and Subtraction: Two approaches To
/ractilitate Gene Discovery, Genome Research 6, 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                      African malaria mosquito.
Anophales gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
                                       1411 GTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 1470
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                                                                                                                                                                                                                                                                                    4A3A-P8G10-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P8G10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fotis C. Kafatos laboratory
Buropean Molecular Biology Laboratory
Meyerhofatrasse 1, 69117 Heidelberg, Germany
Location/Qualifiers
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                                                                                                                               1831 CGGAGCCTATGGAAAACGCCAGCAACGCGGCC 1863
                                                                                                                                                    67 CGGAGCCTATGGAAAAACGCCAGCAACGCGGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P8G10"
                                                                                                                                                                                                                                                                                                                                                                               AJ281661.1 GI:6929540
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CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTCGCAATAAGTCGTGTCTTACCGGCTTG 450	GACTCAAGACGATAGTTACCGGATAAGGCGCAGGGGGGGG	GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGGTTCGTGC 390	ACACAGCCCAGCTIGGAGCGAACGACCIACACAGAATACCIACAGCGIGAGCAT 1650 			GFCGAAACAGGAGGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGT 1770 	CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTCATGCTCGTCAGGGGG 1830	CCINICAGGIIICGCCACCICIGACITGAGCGICGACITTITGIGATGCTCGTCAGGGGGG 150	cusancertarionamanaciecencenegee 1863 			DKFZp434C172_s1 434 (synony: htes3) Homo sapiens DKFZp434C172 3', mRNA sequence.	AL044364 AL044364.1 GI:5432586	EST. human	Euk Mam	I to 954) , Benes,V.	Wiemann,S. EST (Ansorge, Benes, et al.) Unpublished (1999) Contact: Ansorge W	Marklopferspitz 18a D-82152 Martinsried, Germany Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	delberg.de; pratories,	German Genome Project.  No rl sequence available.			/clone_lib="#44 (synonym: htes3)" /tisue_type="testis" /dov_etane="adult="#"	/lab_host="PHIOD" /hote="Vector: pSport1: Site 1: NotT: Site 2: Salt"	• • • • • • • • • • • • • • • • • • •
Db 509	7	Db 449	Qy 1591 Db 389	П		UY 1/11 Db 269	QY 1771	1831	149	RESULT 12	AL044364/c LOCUS	DEFINITION	ACCESSION VERSION	KEYWORDS	ORGANISM	AUTHORS	TITLE JOURNAL COMMENT				FEATURES				BASE COUNT ORIGIN

Score 449.8; DB 10; Length 954; Pred. No. 8.9e-102;

21.2%;

Query Match Best Local Similarity

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AL593919 XGC-gastrula Silurana tropicalis cDNA clone TGas003010 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="tqss003010"
/clone=lib="xcc-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/dab_host="scherichia coli DH108"
/note="vbctor: pCS107; Site_1: EcoRI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-Not1 cut cDNA was then ligated
                                         IGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT 1470
                                                                                                                                                                                                                                                                                                     ARGAAAGCGCCACGCTTCCCGAAGGGAGAAGCGGACAGGTATCCGGTAAGCGCCAGG 1710
                                                                                                                                 IGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG 1530
                                                                                                                                                                                                                    CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGC 1590
                                                                672
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1 (bases 1 to 629)
Huckle, E., Taylor, R., McMurray, A., Ashurst, J.L., Zorn, A.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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  2; Indels
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Sanger Xenopus tropicalis EST project 2001
Unpublished (2001)
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TROPICALIS_SEQUENCE_ID: TGas003010.sp6
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Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropésanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCCTATGGAAAACGCCAGCAACGCGGCC 1863
0; Mismatches
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AL593919
AL593919.1 GI:15005980
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151; Conservative
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
 end and NotI at the 3'
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                                                                                       Length
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                                                                                    Score 448.8; DB 10,
Pred. No. 1.4e-101;
0; Mismatches 2;
into pCS107 with EcoRI at the
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European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, C
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Anopheles gambiae
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AJ281480.1 GI:6929360
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/clone="4434-P468"
/clone="1h="Anopheles gambiae immune competent 4434"
/clone_lib="Anopheles gambiae immune competent 4434"
/cell_line="immune competent 4434"
/lab_host="E. col! immune competent 4434"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: ECORI; Site_2: Not!; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA. The 4A3A is a directionally cloned and normalized cDNA. Ibrary that was constructed from the 4A3A call line oligo-" primed cDNA according to: Bonaldo, Lennon & Soares oligo-" primed cDNA according to: Bonaldo, tennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 609)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.6e-101;
0; Mismatches 3;
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Best Local Similarity 99.3
Matches 450; Conservative
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Bonaido, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

195 c 159 g 127 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not1; Site_2: EcoRI; lst strand cDNA was prepared from mRNA obtained from pooled mammary gland tumors with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                Tissue Procurement: Lothar Hennighausen Ph.D., Jeffrey Green M.D., Gilbert Smith, Ph.D., William Muller, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Pred. No. 1.7e-101;
0; Mismatches 94; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled mammary gland tumors"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:2938635"
/clone_lib="NCI_CGAP_Mam10"
                                                                                                                                                                                                                               Seq primer: -40RP from Gibco
High quality sequence stop: 512.
Location/Qualifiers
Email: cgapbs-r@mail.nih.gov
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Best Local Similarity 84.4%;
Matches 514; Conservative (
                                                                                                                                                                                                                                                                                             609.
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P53 cDNA RT-PCR pr Human lectomedin-2 Human lectomedin-2 Human MBSP2 cDNA c Human truncated pl Alphalib integrin

Forward PCR primer

Perfect score:

Title:

Run on:

Scoring table: Sequence:

Searched:

Database

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Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA sequence comprises a 5' acceptance site of novel humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vector; vaccine; tumour; antigen; plasmid pITL; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised vector 5' sequence acceptance site.
                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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AAF56642
AAF28415
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AAX02029
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 AAV21735;
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rBPI(1-199)-Ala132
Probe/Primer for b
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PCR primer 5'ORF2
Mouse wild type al
Calcium channel al
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17.151 Million cell updates/sec
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(c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Result

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Human interferon-a Codon-optimised HP Human delta-5-desa

Asp2 coding sequen

Murine class II MH Murine signalling Murine signalling Plasmid TKHH2 PCR Murine MHC class I PCR primer #6048 f Ig-betath fusion g Primer #1 Uniden Primer #1 Uniden Frimer #1 Uniden

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comprise a human-derived promoter or mammalian homologue and a sequence acceptance site that is designed to directionally accept sequence specific products from RT-PCR based cloning strategies via a unique site within an interrupted palindrome recognition sequence for a restriction endonuclease which is incorporated into the PCR primer. In this embodiment, the palindrome recognition sequence is for Bgll. The 5' acceptance site reads on the positive strain, and includes a GC sequence recognised by Bgll and an ATG start codon. The 3' GCC moiety keeps the sequence in-frame and vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are companied.
                                                                                                                                                                                                                                                                                                                                                                        generate immune responses to the target sequences with little or no
  polynucleotide vectors such as pITL (see AAV21724).
                                                                                                                                                                                                                                                                                                                                                                                                immune response to the other vector components.
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Gaps ; Length 12; 0; Indels 100.0%; Score 12; DB 19; 100.0%; Pred. No. 7.9e+02; tive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 12; Conservative

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1 GCCACCATGGCC 12 g

AAZ51587 standard; DNA; 19 AAZ51587 RESULT HANDER STANDER STANDER

AAZ51587;

21-JUN-2000 (first entry)

PCR primer 5'ORF1 to amplify human Deltex (hZDX) coding region.

Notch signalling protein; Deltex; hZDX; human; cell differentiation; proliferation; ankyrin repeat; regulator; cytostatic; modulator; cancer; diagnosis; treatment; T lymphoblastic lymphoma; leukemia; lung carcinoma; adenocarcinoma; cervical neoplasia; PCR primer; ss.

Homo sapiens.

WO200012698-A1.

09-MAR-2000.

99WO-GB02802. 25-AUG-1999;

98US-0098512 31-AUG-1998;

(ZENE ) ZENECA LTD.

Kays JS; Khoury-Christianson AM,

WPI; 2000-256639/22.

Novel human cytoplasmic Notch signaling protein and polynucleotide useful for identifying compounds that modulate Notch signaling protein and for diagnosis, treatment of leukemia, T lymphoblastic lymphoma -

Example 2; Page 16; 60pp; English.

The present DNA sequence is the PCR primer, 5'ORF1 used to amplify the coding region from the start site of ORF1 through the common stop codon (479-2347), using human spleen cDNA library as the template. The 5'end PCR primer incorporates a Kozak consensus sequence prior to the ATG codon. The human cytoplasmic Notch signalling protein, Deltex (AZDX), is integral to cell differentiation and proliferation. It binds to the ankyrin repeat region of human Notch receptor and functions as a

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The present DNA sequence is the PCR primer, 5'ORF2 used to amplify the coding region from the start site of ORF2 through the common stop codon (485-2347), using human spleen cDNA library as the template. The 5'end PCR primer incorporates a Kozak consensus sequence prior to the ATG codon. The human cytoplasmic Notch signalling protein, Deltex (hzDX), is integral to cell differentiation and proliferation. It binds to the anythin repeat region of human Notch receptor and functions as a regulator of Notch signalling pathway and has cytostatic activity. hzDX sequence is useful to identify compounds that modulate biological or pharmacological activity of Deltex Notch signalling protein. Specific antisense oligomers and dominant negative mutants are useful for therapeutic purposes. It is also used for diagnosis and treatment of conditions associated with aberrant Notch signalling, like cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation; ankyrin repeat; regulator; cytostatic; modulator; cancer; diagnosis; treatment; T lymphoblastic lymphoma; leukemia; lung carcinoma; adenocarcinoma; cervical neoplasia; PCR primer; ss.
regulator of Notch signalling pathway and has cytostatic activity. hzp. sequence is useful to identify compounds that modulate biological or pharmacological activity of Deltex Notch signalling protein. Specific antisense oligomers and dominant negative mutants are useful for therapeutic purposes. It is also used for diagnosis and treatment of conditions associated with aberrant Notch signalling, like cancers, including T lymphoblastic lymphoma, leukemia, adenocarcinoma, lung carcinoma and cervical neoplasia. The nucleotide sequence is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human cytoplasmic Notch signaling protein and polynucleotide useful for identifying compounds that modulate Notch signaling protein and for diagnosis, treatment of leukemia, T lymphoblastic lymphoma -
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notch signalling protein; Deltex; hZDX; human; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer 5'ORF2 to amplify human Deltex (hZDX) coding region.
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                                                                                                                                                                                                                                                                             DB 21; Length 19;
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; secreted calcium channel alpha2delta subunit; alpha2delta-2; alpha2delta-4; voltage-dependent calcium channel; VDCC; gabapentin; scintillation proximity assay; SPA; nickel flashplate assay; filter binding assay; wheat germ lectin flashplate assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence for deletion mutant PCR primer #1 is used with PCR primer #2 (AASO1418) to obtain mouse alpha2delta subunit deletion mutant from the wild type mouse calcium channel alpha2delta-3 subunit (AAMU01026). The sequence is described in an invention relating to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcium channel alpha2delta subunits, useful in e.g. SPA assays, Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays -
                                                                                                                                                Gaps
carcinoma and cervical neoplasia. The nucleotide sequence is useful for diagnostic assays to detect expression levels of h2DX.
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/note= "Tagged region not present in template"
                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse wild type alpha2delta-3 deletion mutant PCR primer #1.
                                                                                                            Length 19;
                                                                                                                                                0; Indels
                                                                                                        ch 100.0%; Score 12; DB 21; 11 Similarity 100.0%; Pred. No. 8e+02; 12; Conservative 0; Mismatches 0;
                                                      Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                AAS01417 standard; DNA; 23 BP.
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misc_feature
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ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating disorders of the nervous system, including pain, epilepsy anxiety. Sequences AAF57552-555 represent PCR primers related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where the ligands identified are useful for treating disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex; nervous system disorder; pain; epilepsy; anxiety; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gee NS;
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                                                                                                                                                                                                                                      Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcium channel alpha2delta subunit related primer.
                                                                                                                                                                                                                                      100.0%; Score 12; DB 22;
1larity 100.0%; Pred. No. 8.1e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 8.1e+02;
iive 0; Mismatches 0;
                                                                                                                                     Sequence 23 BP; 2 A; 10 C; 9 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dissanayake V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and anxiety. Sequences AAF57552-555 r.
calcium channel alpha2delta subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 104; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system, including pain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF57554 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2000; 2000WO-EP09136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WARN ) WARNER LAMBERT CO.
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                                                                                                                                                                                                                                                                   Local Similarity
es 12; Conserv
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us-09-242-202a-22\_copy\_1\_12.rng

AAQ41717

RESULT

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Polymerase chain reaction; primer; amplify; PCR; plasmid; pING4533; pING4503; bactericidal/permeability-increasing protein. BPI; IgG; heavy; chain; pMB27; fusion protein; Gram negative; renal failure; bacterial infection; endotoxin related shock; metabolic acidosis; disseminated intravascular coagulation; anemia; thrombocytopenia; leukopenia; adult respiratory distress syndrome; hypotension; fever; constant region; lipopolysaccharide complement binding; fever; placental transfer; Fc receptor binding; ss.
                            PE; Pseudomonas exotoxin; influenza A virus; MI; matrix protein; BSK-PEM1; ribosome binding site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6 describes the construction of BSK-PEMI.
BSK-PEMI was made from BS-PEMI by the replacement of the 21 bp
XMOI/HindIII fragment with a 24 bp (sio) fragment encoding a
consensus eukaryotic ribosome binding site. The purpose of the
construct was to increase the yields of in vitro translated PEMI
                                                                                                                                                                                                                                                                                                                                                                                            Bacterial toxin-antigen protein conjugates - to elicit of T-lymphocyte immune response, used for preventing viral infections, e.g. by influenza virus, HIV and human papilloma:virus
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100.0%; Pred. No. 8.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          Hawe LA, Liu MA,
Shi X, Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 6 A; 9 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 24; Page 78; 85pp; English.
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                                                                                                                                                                                           92EP-0202660.
                                                                                                                                                                                                                               91US-0756249.
                                                                                                                                                                                                                                                                                                    Friedman A,
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC
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                                                                                                                                                                                           02-SEP-1992;
                                                                                                                                                                                                                               09-SEP-1991;
                                                                                                                                                                                                                                                                                                    Donnelly JJ,
                                                                                                                                                        17-MAR-1993.
                                                                                                                  EP532090-A.
                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The construct BS-PEMI encodes a hybrid protein comprising domains I and II from Pseudomonas exotoxin fused to amino acids 2-252 of the influenza A virus matrix protein MI. The PE-derived portion of the hybrid protein allows internalisation of the protein by an antigen. Presenting cell. The hybrid protein is then processed and an antigence segment (i.e. the Influenza A virus matrix protein) is presented on the cell surface where it elicits an immune response. BSR-PEMI was made from BS-PEMI by replacing the 21bp XhoI/HindIII fragment with a fragment (i.e. AAQ41717) encoding a consensus eukaryotic ribosome binding site. The purpose of the construct was to increase the yields of in vitro translated PEMI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                     Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus;
matrix protein; Ma; Pseudomonas exotoxin; cell recognition domain;
translocation domain; anti-viral agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA encoding bacterial toxin-antigen conjugates - are useful as vaccines against viral infections, tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marshall MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 14;
100.0%; Pred. No. 8.1e+02;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Liu MA,
Ulmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 6 A; 9 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                                 Consensus eukaryotic ribosome binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hawe LA,
Shi X, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 32; 8Ipp; English.
                                                                                                                        AAQ41717 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                      92EP-0310067.
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                                                                                                                                                                                                  (first entry)
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Oliff AA,
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC
                   3 gccaccatggcc 14
1 GCCACCATGGCC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donnelly JJ, F.
Montgomery DL,
                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1992;
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                                                                                                                                                                                               25-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                12-MAY-1993.
                                                                                                                                                                                                                                                                                                                                              EP541335-A.
                                                                                                                                                              AAQ41717;
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Gaps

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Indels

93WO-US04754.

19-MAY-1993;

25-NOV-1993. WO9323434-A

20-JUL-1993 (first entry)

DX XX XX XX DX XX

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δ q RESULT AAQ37109

Consensus eukaryotic RBS

Length 25;

cytotoxic

Marshall MS;

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11-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                      AAT01078
                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                  The sequences given in AAQ52485-86 are primers which were used in the construction of the rBPI-IgG fusion vector, pING4533. This plasmid contains recombinant bactericidal/permeability-increasing protein contains recombinant bactericidal/permeability-increasing protein contents Sozak sequence given in AAO52487. The rBPI fragment was fused to consensus Kozak sequence given in AAO52487. The rBPI fragment was fused to a constant domain of an IgG heavy chain (HC). Plasmids such as produce fusion proteins which are useful for the treatment of Gram negative bacterial infections and their sequelae including endotoxin related shock and conditions associated with it, such as disseminated intravascular coagulation, anemia, thrombocytopenia, leukopenia, adult respiratory distress syndrome, renal failure, hypotension, fever and metabolic acidosis. Proving BPI or a fragment of it, as part of the fusion with an immuno-globulin heavy chain constant region provides the potential advantages of Fc receptor binding, bivalent binding to lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                  New fusion proteins for treating bacterial infections. - comprising a bactericidal-permeability-increasing protein and a immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BPI; bactericidal-permeability-increasing protein; bactericide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein; Gram-negative bacterium; infection; primer; polymerase chain reaction; PCR; amplification; mutagenesis; protein engineering; cysteine replacement analog; pING4533; consensus Kozak translation sequence; FPBI(1-199)ala132; ss
                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baltaian M, Burke D, Grinna L, Horwitz A, Theofan G;
                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 12; DB 14; 100.0%; Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 BP; 5 A; 10 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                 Example 1; Page 20; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rBPI(1-199)ala132 primer BPI-23.
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           92US-0885911
                                                                                                                           heavy chain constant domain
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Best Local Similarity 100.00
These 12; Conservative
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                                                       Horwitz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCCACCATGGCC 12
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                                                                             WPI; 1993-386485/48
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                                 (XOMA ) XOMA CORP.
          19-MAY-1992;
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                                                       Grinna LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bactericidal-permeability increasing protein; BPI; truncated; dimer;
endotoxic shock; heparin neutralisation; anglogenesis; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      truncated derivative of human mature BPI carrying a C132A mutation, rBPI(1-199) 926115., in which the codon specifying the 5th amino acid of the BPI signal peptide is placed in the context of the consensus Kozak translation initiation sequence (AAQ67275) and the first 4 amino acids of the BPI signal are removed. This is accomplished by PCR amplification of BPI CDNA using primers BPI-23 (AAQ67276) and BPI-2 (AAQ67277).
                                                                           Bactericidal-permeability-increasing protein analogues with $$15.12 or Cysl35 replaced - also fusion proteins and C-terminally truncated forms, have increased stability and are useful to treat gram-negative bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rBPI(1-199)-Ala132 (with 27 amino acid signal) PCR primer BPI-23.
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                                                                                                                                                                                                                                                                                                                                                                Plasmid pING4533 contains a DNA insert encoding a C-terminally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 12; DB 15;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 5 A; 10 C; 9 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                Disclosure; Page 11; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT01078 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0212132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0212132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ammons WS, Little RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCCACCATGGCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 gccaccatggcc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-319904/41.
WPI; 1994-279744/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA ) XOMA CORP.
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BP.

AAT84743 standard; DNA; 27

AAT84743 RESULT

AAT84743;

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Gaps

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10 gccaccatggcc 21

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Recombinant endotoxin-binding protein comprising bactericidal/permeability increasing protein (BPIP) or its endotoxin N-terminal fragment, can be produced by growing genetically transformed host rells in a suitable medium so that BPIP is secreted into the medium. The BPIP is then isolated and can be used to control bacterial infections. The same method can be used where BPIP is replaced with structurally related protein. Inmulus anti-LPS factor, tachyplesin or structurally related protein. This sequence is reproduced in the
                                                                                                                                                                                                                                                                                                                                                                                                                       Probe/Primer for bactericidal/permeability increasing protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recovery of recombinant endotoxin binding protein - by culturing transformed cells in medium contg. cation exchange material, useful for treatment of bacterial infections.
first 4 amino acids of the BPI signal peptide are removed; the codon specifying the fifth amino acid of the signal sequence (Met at position -27) is placed in the context of a consensus Kozak translation initiation sequence. The truncated rBPI is suitable for dimerisation in the presence of copper 2+ ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           permeability increasing protein; BPIP; infection;
                                                                                                                                                      Length 27;
                                                                                                                                               100.0%; Score 12; DB 16; Length 2' 100.0%; Pred. No. 8.1e+02; 'Ive 0: Mismatches 0; Indels
                                                                                                 Sequence 27 BP; 5 A; 10 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 BP; 5 A; 10 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 21; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification but is not referred to.
                                                                                                                                                                                                                                                                                                                             AAQ97620 standard; cDNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0885501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0072063.
                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1996 (first entry)
                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control; recombinant; ss
                                                                                                                                                                                                                                 10 gccaccatggcc 21
                                                                                                                                                                                                                1 GCCACCATGGCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-283094/37.
                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bactericidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5439807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grinna LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                             AA097620;
                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                               AAQ97620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid fusion protein for treating Gram-negative bacterial infections - comprising bactericidal/permeability increasing protein and immunoglobulin heavy chain constant domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                     Primer BPI-23 for bactericidal permeability increasing protein DNA.
                                                                                                                               Primer; polymerase chain reaction; PCR; amplification; Ig; BPI; immunoglobulin; heavy chain; constant region; plasmid phB27; preparation; hybrid; fusion; bactericidal permeability increasing; treatment; Gram-negative; bacterium; bacteria; infection; endotoxic shock; disseminated intravascular coagulation; anaemia; thrombocytopaenia; thrombocytopenia; leukopenia; adult respiratory distress syndrome; ARDS; renal failure; hypotension; fever; metabolic acidosis; ss.
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                                                                                                                           Primer; polymerase chain reaction; PCR; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 18;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 5 A; 10 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Columns 35-36; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ġ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and increased placental transfer.
                                                                                                                                                                                                                                                                                                                                                                                                   92US-0885911.
                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0064693,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0885911
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grinna LS, Horwitz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-350186/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCCACCATGGCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA ) XOMA CORP.
                                                       03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1993;
19-MAY-1992;
                                                                                                                                                                                                                                                                                                                         US5643570-A.
                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997
                                                                                                                                                                                                                                                                                         Synthetic.
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10 gccaccatggcc 21

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Gaps

; 0

Indels

Length 27;

100.0%; Score 12; DB 16; 100.0%; Pred. No. 8.1e+02; tive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 12, Conservative

1 GCCACCATGGCC 12

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vascular disease; lectomedin-2; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96037
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                                                                                                                                                                                                                                                                                                                           Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  RT-PCR primer 1 and RT-PCR primer 2 (see AAV21729) were used to amplify a portion of p53 cDNA (see AAV21730). The primers include mutated sequences that allow the amplified product to be incorporated into vectors such as plasmid pITL (see AAV21724). Novel humanised vectors, which can be based on piTL, comprise a human derived promoter (or mammalian homologue) which is functional in mammalian target tissue and cells and a sequence acceptance site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 7-transmembrane receptor; lectomedin; lectin-binding; mucin; olfactomedin; cellular adhesion; atherosclerosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                which accepts CDNA products from RT-PCR cloning. The vectors are non-replicating in mammalian cells but are capable of extended stable expression of the target sequence, generating an immune response in immunised individuals. The vectors selectively elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune responses to the target sequences with little or no immune response to the other components of the vectors. The vectors are particularly useful in accompdating monomorphic and polymorphic nucleic acid sequences encoding tumor antigens via PCR technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                          Vector; vaccine; tumour; antigen; plasmid pITL-hHER/neu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lectomedin-2 clone 2-1 amplifying primer JD#1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 19;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 3 A; 13 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                     human; p53; cancer; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 47; 125pp; English.
 ВР
                                                                                                                                                                                                           97WO-US14306
AAV21728 standard; cDNA; 27
                                                                                                                                                                                                                                 96US-0023931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ28010 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2000 (first entry)
                                            17-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                  P53 cDNA RT-PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCCACCATGGCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-159552/14.
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                         14-AUG-1997;
                                                                                                                                                                                                                                 14-AUG-1996;
                                                                                                                                                            WO9806863-A1
                                                                                                                                                                                   19-FEB-1998.
                                                                                                                                                                                                                                                                                EĽ,
                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ28010;
                    AAV21728;
                                                                                                                                                                                                                                                                                Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ID AAZ2

XX AAZ

XC AAZ2

XX DT 05-J.

XX W Huma

KW Huma
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The invention provides purified and isolated human 7-transmembrane receptor lectomedin polypeptide or its fragments. The lectomedin polypeptide or its fragments. The lectomedin-like and mucin-like domains. The polypeptide can be produced by standard recombinant methodology. The polypeptide is involved in cellular adhesion and cytoplasmic metabolic pathways that are modulated by extracellular signaling. Specific binding to lectomedin. Expressed on smooth muscle cells may be required for proliferation of these cells in atherosclerosis. The polypeptide is used to raise specific antibodies, and to identify specific mining agents that modulate (increase or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            decrease) its activity. The lectomedin nucleic acids are used as source of probes and primers, and of therapeutic antisense, riboxyme or triplex-forming agents, and in gene therapy to restore deficient lectomedin activity. Specific binding agents of lectomedin are are used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases that involve lectomedin activity, e.g. vascular diseases such as atherosclerosis. The present sequence represents a primer for amplifying a human lectomedin-2 clone 2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiatherosclerotic; vasotropic; cytostatic; gene therapy; atherosclerosis; restenosis; vascular disease; peripheral neuropathy; cancer; nerve regeneration; renal cystic epithelium; uterine implantation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human lectomedin receptor polypeptide, used to identify specific binding partners for treating e.g. vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lectomedin; seven transmembranė receptor protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12; DB 20;
Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 6 A; 10 C; 6 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lectomedin-2 cDNA 2.1 PCR primer JD#1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 36; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA96037 standard; DNA; 28 BP.
                                                                                                                                                                                                                                                                                                                98US-0076782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCCACCATGGCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-571596/48.
                                                                                                                                                                                                                                                                                                                                                                                 ICOS-) ICOS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                         04-MAR-1998;
                            Homo sapiens
                                                                                                W09945111-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayflick JS;
                                                                                                                                                                    10-SEP-1999
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA96037;
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The present sequence is a PCR primer which was used in a procedure for isolating human seven transmembrane receptor lectomedin polypeptides. The polypeptides have a characteristic extractular structure including lectin-binding, olfatcomedin-like and mucin-like domains. Modulator compounds that inhibit the binding of lectomedin to a binding partner (galectin-3) may be used to treat conditions such as atherosclerosis, restenosis, vascular disease, peripheral neuropathy, cancer, nerve regeneration, and pathologies of the renal cystic epithalia and uterine implantation. Nucleotide sequences encoding the lectomedin polypeptides or useful in gene therapy. The lectomedin polynucleotides and polypeptides may be used to identify lectomedin binding partner compounds. The polynucleotides are useful for detecting lectomedin cexpression in cells and for identifying genetic mutations in the lectomedin genes. Antisense lectomedin nucleic acids are able to inhibit expression of lectomedin genes.
                                                                                                                                                                                                                                                                                           Isolated human seven transmembrane receptor lectomedin polypeptide or its fragment, useful for identifying agents which can treat atherosclerosis, restenosis or vascular disease .
                                                                                                                                                                                                                 Douangpanya J, Puri KD;
                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 42; 241pp; English.
                                                                                     03-MAR-2000; 2000WO-US05934.
                                                                                                                              99US-0262537.
                                                                                                                                                                                                               Hayflick JS, Fox RD,
                                                                                                                                                                                                                                                      WPI; 2000-579274/54.
                                                                                                                                                                        (ICOS-) ICOS CORP.
WO200052039-A2.
                                                                                                                              04-MAR-1999;
                                           08-SEP-2000
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Gaps ; 0 100.0%; Score 12; DB 21; Length 28; 100.0%; Pred. No. 8.1e+02; Ative 0; Mismatches 0; Indels Query Match 100.0 Best Local Similarity 100.0 Matches 12; Conservative οχ

Sequence 28 BP; 6 A; 10 C; 6 G; 6 T; 0 other;

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1 GCCACCATGGCC 12  Search completed: January 17, 2002, 12:03:54 Job time: 17821 sec

Sequence:

Title:

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Searched:

Database

Result

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AA214420 zq91h04.r
AA714853 vu62c06.r
N50245 yy84c04.r1
BI152476 602915613
AU083189 AU083189
AA784758 92b06a1.r
BG17633900 602075263
BG921952 60282638
BG921952 60282638
BG921952 6021010476
AZ225473 RPCI-23-7
BG288593 602406535
BE286612 601110476
AA749848 ISARO373
BE366298 PIL 32-H1
                                                                                                                                                                                                                                                                                                                                                                                                                 BIO78628 49 bp mRNA EST 20-JUN-2001 602872729F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5004750 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E langering roughlary Schilogharing Millings, Mullings, Mullings, Mullings, Mullings, Mullings, Mullings, Mullings, Mullings, I to 49)

NIH-MGC http://mgc.nci.nih.gov/.

Lunpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LANL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1043 row: i column: 07

High quality Sequence stop: 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                         AA750627
BF911674
AA279415
                                                                                                                                                                                                                            AI864485 1
BE266769 1
BE736479 1
                                                                                                                                                                                                                                                         AI715931 UBE746616 AZ069587 BE269092
                                                                                                                                                                                                       BE294646
BE270281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 49
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                                                          AA784758
BG176372
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BE270281
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BE269092
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                                                                               BF533900
                                                                                           BG921952
                                                                                                                        BG282693
                                                                                                                                                                           AA750627
                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BIO78628
BIO78628.1 GI:14496958
house mouse.
                                      RESULT 1
BIO78628/C
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BF166238 601776892
BG242301 602354472
BG259484 602378587
BE376022 601229459
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PM3-CN010
CM3-EN019
og91f04.s
RC0-TN007
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IL5-GN023
                                                                              (without alignments)
19.834 Million cell updates/sec
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                                                                     Search time 6501.33 Seconds
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                                                                                                                                                                                                        22703874
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                    11351937 segs, 5372889281 residues
                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                          US-09-242-202A-22_COPY_1_12
                                                                     January 17, 2002, 08:54:19
                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BG242301
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                                                OM nucleic - nucleic search, using sw model
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em_gss_vrt:*
em_gss_other:*
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em_estbal:*
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em_estco:*
em_btc:*
gb_estl:*
gb_htc:*
gb_htc:*
em_gss_tun:*
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Maximum DB seq length: 200000000
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601176344 601186087 QV1-UT009

ISGS0207

wj93a01.x

RPCI-23-4 1M0030M20

RC3-BN042 601184257

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Query Match
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BG242301/c
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                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9269 row: g column: 23
High quality sequence stop: 50.
Location/Qualifiers
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Stem call origin."
/lab_host="DH108"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF166238.1 GI:11046590
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Best Local Similarity
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BG242301 56 bp mRNA EST 13-FEB-2001
602354472F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483048 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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6023788871 NIH_MGC_92 Home sapiens CDNA clone IMAGE:4509501 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.go.row: o column: 17
                                                                                                                                                                                                                                                      1 (bases 1 to 56)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Location/Qualifiers
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BG259484
BG259484.1 GI:12769300
                                                                                                      BG242301.1 GI:12752116
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                                                       mRNA sequence.
BG242301
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                                                                                                                                                                                                                               /db_xref="taxon:0506"
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/clone="INAGE:4509501"
/clone="INH_MGC_92"
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Site_2: Sal1; Cloned unidirectionally; Oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NH-MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE376022 99 bp mRNA EST 21-JUL-2000 601229459F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3593462 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 99)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 2.2e+04;
tive 0; Mismatches 0;
                                                                                                  http://image.llnl.gov
plate: LLAM10389 row: m column: 22
High quality sequence stop: 91.
Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
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BE376022
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Matches 12; Conserv
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JOURNAL
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SOURCE
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Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langidge, P., Lazo, G. R., Lin, J.J., McGultre, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae Expressed Sequence Tags for Species of the Triticeae

L. Unpublished (2000)

Contact: Langridge P

Special Research Centre, Basic and Applied Plant Molecular Biology Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA Tel: 61 8 8303 7368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
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/done="taxon:4565"
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/tissue_type="excised florets:
/tissue_type="excised florets:
/dev_stage="meiotic stage no later than metaphase I"
/note="Vector: pSport I (Life Technologies cat. no.
18448-013); Site_1: Sall; Library constructed in pSport I.
Directionally cloned using the Superscript Plasmid System
for cDNA synthesis and plasmid cloning. M13 Reverse
sequencing primer used to obtain 5' sequence data. 1.4
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1 (bases 1 to 99)
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AWB009.G08F000328 ITEC AWB Wheat Meiotic Stage Library Triticum
aestivum cDNA clone AWB009.G08, mRNA sequence.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 27\ c 44\ g 7\ t
                                                                                                                                                                                                                                           Gaps
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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100.0%; Pred. No. 2.2e+04;
Live 0; Mismatches 0;
                                                                                                                                                                             Score 12; DB 10;
Pred. No. 2.2e+04;
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Kbp average insert size."
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100.0%;
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Best Local Similarity 100.0
Matches 12; Conservative
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Matches 12; Conservative
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS MEDLINE

COMMENT

JOURNAL

TITLE

BG006903/c

RESULT

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
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/note footh: Female C57BL/6J mouse footh
/note fo
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1 (bases 1 to 115)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 110)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mogann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from lease contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieterédéjong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 321 row: E column: 6
Seq primer: SP6
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PM3-CN0100-230101-002-h05 CN0100 Homo sapiens CDNA, mRNA sequence.
BG980184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                         Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-321E6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
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100.0%; Pred. No. 2.2e+04;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-GN0239-271100-273-910_18*t3=2000-11-27$t4=1)
Seq primer: puc lB forward
High quality sequence stop: 101.
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RPCI-23-321E6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-321E6,
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                              24-JAN-2001
                                                                                                              BG006903 101 bp mRNA EST 24-JAN-20
IL5-GN0239-271100-273-910_1 GN0239 Homo sapiens CDNA, mRNA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="GN0239"
/dev_stage="Adult"
                                                                                                                                                                                                                                     BG006903
BG006903.1 GI:12450544
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Best Local Similarity 100.9
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FEATURES

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RESULT AQ978348

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ACCESSION VERSION KEYWORDS SOURCE

Length 110; Indels

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/organism="Homo saplens"
/organism="Homo saplens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/dev_stage="Adult"
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/note="Organism inng_normal; Vector: pucl8; Site_1: SmaI;
/note="Organism inng_normal; Vector: Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be set in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0194-151200-563-g04&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence start: 25
High quality sequence stop: 117.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 12; DB 11; Length 117; 100.0%; Pred. No. 2.2e+04; ive. 0; Mismatches 0; Indels (
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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/clone_lib="NCI_CGAP_Kid5"
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/db_xref="taxon:9606"
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: colon_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under the pure products of the publication of the publication were performed under th
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PM3&t2=PM3-CN0100-230101-002-h05&t3=2001-01-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 114.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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       Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                                    δλ
                                    Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RCO-TN0079-150 900-026-hlg.ts12-2000-09-15&t4=1)
Seq primer: puc 18 forward: 31
High quality sequence start: 31
High quality sequence stop: 124.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dcone_lib="Tw00079"
/dev_stage="Adult"
/note="Organ: testis_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products Site_2: SmaI; A mini-library was made by cloning products Site_2: SmaI; A mini-library was made by cloning products of serived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveire, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF092125 124 bp mRNA EST 19-OCT-2000
RCO-TN0079-150900-026-hll TN0079 Homo sapiens CDNA, mRNA sequence.
BF092125
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                               Gaps
/tissue_type="2 pooled tumors (clear cell type)"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                                                   Length 124;
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 12; DB 10; 100.0%; Pred. No. 2.2e+04;
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                  /lab_host="DH10B
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Matches 12; Conserv
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ORGANISM

SOURCE

REFERENCE

AUTHORS

JOURNAL MEDLINE

COMMENT

TITLE

FEATURES

ACCESSION VERSION KEYWORDS

RESULT 1 BF092125

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/note="Vector: pBluescript II SK+; Site_I: EcoRI; Site_2:
XhoI; The CDNA library wms constructed from mRNA isolated
from 2.3 week old seedlings that were induced for symptoms
of SDS (Sudden Death Syndrome) disease by the
translocation of culture filtrate of Fusarium solani f.
Sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
567374 is partially resistant to the disease SDS. Plant
tissue (expanded leaves, folded leaves, and new shoots)
were collected at 1, 6, 24, and 48 hrs. after inoculation
and their mRNA pooled equally for cDNA construction. The
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG511069 126 bp mRNA EST 28-MAR-2001 sac65d66.y1 Gm-c1072 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1072-179 5' similar to SW.NUO2_SOLTU P80268 NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobases 1 to 126)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Maylie,T., Underwood,K., Steptco,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Kitter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,P.,R., Waterston,R. and Wilson,R.
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com.
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:3847"
/clone="GRNOME SYSTEMS CLONE ID: Gm-c1072-179"
/clone_lib="Gm-c1072"
                                                                                                                                                                          Length 124;
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Public Soybean EST Project
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Score 12; DB 10;
Pred. No. 2.2e+04;
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poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion wis methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois).

28 a 34 c 34 g 30 t
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(bases 1 to 127)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dierrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Fullman,M., Kucaba,T., Le,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevsskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zgg1h04.rl Stratage hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649399 5' similar to contains Alu repetitive element;, mRNA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 Ef from Amersham
High quality sequence stop: 116.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Gaps
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/db_xref="GDB:5278679"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 130)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
vu62c06.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1195978 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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100.0%; Pred. No. 2.2e+04;
iive 0; Mismatches 0;
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:1195978"
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Search completed: January 17, 2002, 08:54:22 Job time: 7134 sec

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January 17, 2002, 11:49:54; Search time 10436.3 Seconds (without alignments) 2445.411 Million cell updates/sec
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1547
1 GGTACCTGCCACCATGGCGC......CTCGCACAGCCTCTCCCACA 1547
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	L08875 PiAN7 clon1 V00089 Cloning vec	X14353 Plasmid pi-	L08918 Pi-VX cloni 107209 Sequence 3	AB009864 Expressio	AXUU32Ub Sequence Z50148 Artificial	A60212 Sequence 8	AA122200 Sequence A60209 Sequence 5	AR122285 Sequence	AR122286. Sequence	A60211 Sequence 7	AX027785 Sequence	AR038307 Sequence	158596 Sequence 15	158610 Sequence 17 AR027070 Sequence	186203 Sequence 9	AF087567 Cloning v AF086840 Cloning v	AF086841 Cloning v	AF086842 Cloning v	AF086844 Cloning v	AF086845 Cloning v	AFU85846 Cloning v AFU86847 Cloning v	AF086848 Cloning v	AF086849 Cloning v	AF086851 Cloning v	AF086852 Cloning v	AF086853 Cloning v	AF08/562 CLOUING V AF087563 Cloning v	AF087564 Cloning v	AF087565 Cloning v	AFU8/566 Cloning v	AF087665 Cloning v			2001-1111-3C	66T-700-07					to GenBank	IACOL FLOGIAM. FIANA		
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1-202 202- 1 (c) Tyr-tRNA synthetic (GenBank(50):EcoTgy)
198-225 1-28 part 1 of pUCB/M13mp8-polyllinker
234-239 31-36 part 2 of pUCB/M13mp8-polyllinker
240-880 2522-3162 pBR322
                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYLINKER ECORI-Smal-BamHI-Sall-Pstl-BglII-Xbal-HindIII SELECTION
                                                                                                                                   COMMENT
                                                                        #citation sequence information from New England Biolabs COMMENT Obtained 12-SEP-1986 from New England Biolabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGT 933
                                                                                                                                                                                                                                                                                     VecBase(3):pBR322, VecSource(3):Poly8, GenBank(50):EcoTgy
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                                                                                                                                                                             The polylinker of PiAN7 contains additional BglII and XbaI sites within the M13mp8/pUC8 polylinker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 TTTCGGACTTTTGAAAGTGATGGTGGTGGTGGAAGGATTCGAACCTTCGAAGTCGATGAC
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                                                                                                                   Revised 16-DEC-1986 by F. Pfeiffer:
449/450 'AT' to 'TA' to match revised sequence of
PiAN7 is thought to replace PiVX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #checksum 9656
                                                                                                                                                                                                                                                                                                                                                                                                            Conflict (cfl) and Mutations (mut): none
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Pred. No. 6.3e-207;
0; Mismatches 10;
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/db_xref="taxon:32630"
1 239 c 236 g 217 t
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                                                                                                                                                                                                                                                                                                                   Features of PiAN7 (885 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
#sequence 16-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.5%;
Best Local Similarity 95.9%;
Matches 805; Conservative (
                                                                                                                                                                                                                                                          VecBase(3):PiVX
                             artificial
                                                                                                     by magnetic tape
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               ACCESSION VB0066
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ATPIVX 902 bp DNA SYN 28-SEP-1992 Cloning vector pi-VX used for screening bacteriophage lambda gene libraries for specific DNA sequences in Escherichia coli. Probe sequences are inserted in the vector pi-VX. Contains a polylinker, and origin of replication (derived from pMB1) and a tyrosine amber-suppressor gene (synthetic supF gene).
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                                                                                CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGG 1053
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TCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT 480
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                               cloning vector; origin of replication; plasmid; polylinker;
                           AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAACCGCTGCG
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/organism-"Cloning vector pi-VX"
//db_xref="taxon:31856"
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/plasmid="pi-vx"
/db_xref="taxon:32630"
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/note="polylinker"
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Best Local Similarity 98.1
Matches 790; Conservative
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                                                                                        CGATGACGGCAGATTTAGAGTCTGCTCCTTTGGCCGCTCGGGAACCCCACCACGGGTAA
                                                   GCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGCGGTTTTTC
                                                                                                                                                                                                   CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG
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                                                                                                                                                                                                                                                                     531 CGATGACGCCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGTAA 590
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                                                                                                                                                                                                  471 CGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGGAAGGATTCGAACCTTCGAAGT
                                                                                                                                                                                                                   12;
                                                                                                                                   Length 902
                                                                                                                                                                    Indels
                                                                                                                               Score 756.2; DB 12;
Pred. No. 2e-204;
0; Mismatches 3;
                                                 replication"
g 223 t
110. .212 /
/note="suppressor tRNA"
213. .902
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                                                 238 c
                                 213. .902
/note="origin
                                                                                                                                 48.9%;
98.1%;
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VecBase(3):pBR322, GenBank(50):EcoTgy, VecSource(3):OriMB1
                 #offspring
                                                                                         residue
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                                                                                                                                                                                                                Obtained from VecBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Currator Program. Pi-VX
Cloning vector used for screening bacteriophage lambda ENTRY PIVX
#TYPE DNA CIRCULAR
TITLE Pi-VX - Cloning vector used for screening bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purification of genomic sequences from bacteriophage libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic and Physical Studies on the replication of ColEl-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The ATCC strain 39083 contains PiVX in combination with plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence given for pBR345 differs at one position from that of pBR322. This may be a sequencing error.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The origin of replication is derived from pMB1 via pBR345 and pKB413. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Backman K., Betlach M., Boyer H.W., Yanofsky S.
Cold Spring Harb Symp Quant Biol 43, 69-76 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USED FOR SCREENING BACTERIOPHAGE LAMBDA GENE LIBRARIES FOR SPECIFIC DNA SEQUENCES IN ESCHERICHIA COLI. PROBE SEQUENCES ARE INSERTED IN THE VECTOR PI-VX. CONTAINS A POLYLINKER, AND ORIGIN OF REPLICATION AND A TYROSINE AMBER-SUPPRESSOR GENE (SYNTHETIC SUPF GENE).
                                               26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION ORIGIN OF REPLICATION KEYWORDS
                                    SYNPIVXV 902 bp DNA circular SYN 26-JUL-1993
Pi-VX cloning vector used for screening bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Maniatis T., Fritsch E.F., Sambrook J.
#book (IN) Maniatis T., Fritsch E.F., Sambrook J.;
MOLECULAR CLONING: 353-361;
COLD SPRING HARBOR LABORATORY (1982).
#comment BASES 1 TO 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Seed B.
#journal Nucl. Acids Res. (1983) 11: 2427-2445
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                                                                                                                          Synthetic construct DNA. synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE artificial COLLECTION ATCC 39083
                                                                                                                                                                                                                                                                                                                                                                 DATE 17-DEC-1982
ACCESSION VB0010
                                                                                                                                                              artificial sequence.
1 (bases 1 to 902)
Gilbert, W.
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L08918.1 GI:310786
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#journal
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                                                   DEFINITION
ACCESSION
                                                                                                                                             ORGANISM
                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
COMMENT
RESULT
SYNPIVXV
                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                             REFERENCE
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1-34 pBR322
1-115 PIVX-Polylinker
207-1 (Constant Synthetic (GenBank(50):EcoTgy)
1-583 OTIMB1
2522-3104 pBR322
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                                                                                                                                                                                                                                                                                                                                                                                                              48.9%; Score 756.2; DB 12; Length 902; 98.1%; Pred. No. 2e-204; Live 0; Mismatches 3; Indels 12;
                                                                                                                                                                                                                                                                           #checksum 9265
VecBase(3):PiAN7, VecBase(3):mWB2344
                                                                                                                                                                                                                                                                                                   1. .902
/organism="synthetic construct"
/db_xref="taxon:32630"
a 250 c 237 g 223 t
                                                                                                                                 Conflict (cfl) and Mutations (mut):
PiVX source
                                                                                                                                                            cfl 811-12 T.C TAC 492-94 OriMB1 cfl 811-12 T.C TAC 3013-15 pBR322
                                                                                                                                                                                                                                                      #Suppressor SupF
SUMMARY PivX #length 902
                           Features pf Pivx (902 bp)
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                             source
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                                                      4- 37
1-115
111-317
320-901
320-901
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Direct Submission
Submitted (16-DEC-1997) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, The Institute of Medical Science, University of Tokyo,
Department of Virology; 4-6-1, Shirokanedai, Minatcku, Tokyo 108,
Japan (E-mail:ssugano@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
                         AGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACT 1008
                                                                              ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA 1128
                                                                                                                                                                                      ACTACGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                                                                TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA 328
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Expression vector pME18S-FL3, complete sequence.
AB009864
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Pred. No. 6.6e-176;
O; Mismatches 288;
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Maruyama, K. and Sugano, S.
PME18S-FL3: a versatile expression vector
Published Only in Database (1997) In press
Location/Qualifiers
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/organism="vectors"
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artificial sequence.
1 (bases 1 to 3392)
Maruyama, K. and Sugano, S.
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Seed, B.D.D.O.M.B., Allen, J., Aruffo, A., Camerini, D., Lauffer, L.D., Quendo, C.P., Simmons, D., Stamenkovic, I. and Stengelin, S.D.
Rapid immunoselection cloning method
Patent: EP 0330191-A2 3 30-AUG-1989;
                                                                                                       AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 1130
                                                   TACGCCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCAAGCCAGTTACCTTC 1190
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             GTCGATGACGGCAGATTTAGAGTCTGCTCCTTTTGGCCGCTCGGGAACCCCACGGGT
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Pred. No. 4.4e-204;
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                                            350 GIGAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCT---
                                 AGCCGGCGCTTTACTGGCACTTCAGGAACAAGGGGCGCCCTTAAGGGCCATATGGTGAGT
                                                                                                                       290 TGTAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGATGAGTA
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                                                                               ----CTTGACCCCAGGGGGGATGGGGGAGACC
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AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGT
                                                                                    1088 ATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTAGCTCTTG
                       ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG
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synthetic construct
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1 (bases 1 to 722)
Carroll,M.W. and Mitrophanous,K.
Equine infectious anaemia virus (ciav) based
Patint: WO 9932646-A 57 01-JUL-1999;
CARROLL MILES WILLIAM (GB); MITROPHANOUS KYRIACOS
LOCATION/Qualifiers
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/db_xxref-"taxon:32630"
/note-"complete sequence of psc65"
1686 c 1751 g 1873 t
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Pred. No. 5.5e-162;
0; Mismatches 16;
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Sequence 57 from Patent WO9932646.
                                                                                                                                     1274 GCGCAGAAAAAAGGATCT 1292
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Best Local Similarity 97.5%;
Matches 617; Conservative
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KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
QLQGSLAALTSLTSITGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAWSR
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YGLLALYALMQFLCAPVLGALSDRFGRRPVLLASLLGATIDYALMATPVLMILTAG
RIVAGITGATGAVGAVAATIADITDGEDRARHFGLMSACFGVGWVAGPVAGGLLGAISLH
APFLAAAVLNGLNLLGGFLMQESHKGERRPMILRAFNVSSFRWARGMTIVAALMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-JUL-1995) Rainer Haas, Infektionsbiologie,
Max Planck-Institut fuer, Biologie, Spemannstr. 34, Tuebingen,
B.W., D-72076, Germany
3 (bases 1 to 2538)
Kahrs.A.F., Odenbreit,S., Schmitt,W., Heuermann,D., Meyer,T.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An improved TnMax mini-transposon system suitable for sequencing, shuttle mutagenesis and gene fusions Gene. 167 (1-2), 53-57 (1995) 96144248
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1767. .2507
/note="replication origin of plasmid pBR322 (oricolE1)"
2508. .2537
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                                                                                   Improved TnMax mini-transposon system suitable for sequencing shuttle mutagenesis and gene fusions Gone (1995) In press 2 (bases 1 to 2538)
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                                             5482 AGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
                            ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCAAGCCAGTTACCTTCGGAAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="pMin1, tetracyclin~resistance protein"
/protein_id="CAA90509.1"
/db_xref="GI:1052555"
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/lab_host="Escherichia coli K12"
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                                                                                                                                                                                                                                                                                                         plasmid; tetracyclin-resistance protein.
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/evidence=experimental
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/transl_table=11
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1 (bases 1 to 2538)
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            Length 2538;
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collins,M.K., Weiss,R.A., Takeuchi,Y. and Cosset,F.
Expression Systems
Cancer.WO 9708330-A 8 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
Location/Qualifiers
1.5865
/organism="unidentified"
/db_xref="taxon:32644"
NT 1492 a 1602 c 1390 g 1373 t 8 others
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, 605.8; DB 12;
. No. 1.6e-161;
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                                                           595 INTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGCCGCTG 654
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1 (bases 1 to 5865)
Collins, M.KatherineLevinge, Weiss, R.Anthony, Takeuchi, Y. and
                                                                                                                             655 TAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTTCCATA
                                                                                                                                                                CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG
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Patent: US 6165715-A 8 26-DEC-2000;
Location/Qualifiers
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                        39.1%;
91.4%;
                                 Best Local Similarity 91.4 Matches 638; Conservative
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Collins,M.K., Weiss,R.A., Takeuchi,Y. and Cosset,F. Expression SYSTEMS
Patent: WO 9708330-A 5 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
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Sequence 5 from Patent W09708330,
A60209
A60209.1 GI:3715217
/organism="unknown"
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Best Local Similarity 91.4%;
Matches 638; Conservative
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1 (bases 1 to 6028)
Collins, M. Katherine Levinge, Weiss, R. Anthony, Takeuchi, Y. and
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Sequence 5 from patent US 6165715.
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/organism="unidentified"
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Pred. No. 3.9e-161
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Patent: US 6165715-A 5 26-DEC-2
Location/Qualifiers
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1 (bases 1 to 6061)
Collins,M.K., Weiss,R.A., Takeuchi,Y. and Cosset,F. EXPRESSION SYSTEMS
Patent: WO 9708330-A 6 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
                                                                                      8 others
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Collins, M. Katherine Levinge, Weiss, R. Anthony, Takeuchi, Y. and
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Patent: US 6165715-A 6 26-DEC-2000;
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Collins,M.K., Welss,R.A., Takeuchi,Y. and Cosset,F. EXPRESSION SYSTEMS
Patent: WO 9708330-A 7 06-WAR-1997;
CANCER RES CAMPAIGN TECH (GB)
LOCATION/Qualifiers
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Database

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Vector; vaccine; tumour; antigen; plasmid pITL-A; ds.
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/note= "ColEl origin of replication"
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/note= "RANTES promoter"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result

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polynucleotide vectors. The vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH polynucleotide vectors. The vector in Escherichia coli DH luman derived promoter or mammalian homologue which is functional human derived promoter or mammalian homologue which is functional no mammalian target tissue and cells and a sequence acceptance site (see AAV21715-536) which accepts cDNA products from RT-PCR cloning. They also contain minimal non-human components, such as a replication or repeits and selectable marker gene (see AAV2171-18) that are necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and appropriately
                                                                                                                                                               Humanised polynucleotide vectors - comprising human derived promorand sequence acceptance site, used for the production of vaccines
                      HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presented on antigen presenting cells.
                                                                                                                                                                                                                                     Claim 14; Page 56-57; 125pp; English.
                        DEPT HEALTH
                        SO ( HSSO)
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Sequence 1547 BP; 344 A; 408 C; 425 G; 370 T; 0 other;

ô 420 TATCAGTGATAAAGTGTCAAGCATGACAAAGTTGCAGCCGAATACAGTGATCCGTGCCGG 120 Gaps GGTACCTGCCACCATGCCGCGGATTCTTTATCACTGATAAGTTGGTGGACATATTATGTT CCCTGGACTGTTGAACGAGGTCGGCGTAGACGGTCTGACGACGCACACGCGGAACG GTTGGGGGTGCAGCCGCCGCGCTTACTGGCACTTCAGGAACAAGGGGGGGCGCCTTAAGG CGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAAGTCGATGACGGC gttggggggtgcagcagccggcgctttactggcacttcaggaacaagcgggcgccttaagg GCCATATGGTGAGTGGATGCCTTGACCCCAGGCGGGGATGGGGGAGACCTGTAGTCAGAG gecatatggtgagtggatgccttgaccccaggcggggatgggggggagacctgtagtcagag ccccggggcaggccaatgcccgtccttcccctgcaggatgagtggtggctc TCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGTT GCATCATTTTGTCTGACTAGGTGTCCTCTATAATATATAAAGCTTGATATCGAATTCTTT gcatcattttgtctgactaggtgtcctctataatattataagcttgatatcgaattcttt ; DB 19; Length 1547; 0; Indels 0; Mismatches 100.0%; Score 1547; 100.0%; Pred. No. 0; Matches 1547; Conservative Best Local Similarity Query Match 61 61 181 241 361 421 121 121 181 301 301 361 421 481 ŏ g QΥ g ŏ 셤 Óλ g Q qq οy Dρ ά g ÓΫ q Qγ

1020 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAACAGGATTAGCA 1080 9 720 780 840 960 960 AGCACCAGATTACGCGCAGAAAAAAGGATCTGGGGGATCCGGAGAGCTCACTCTAGATG GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG GACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCCTCTTCCGA CCCTGCCGCTTACCGGATACCTGCCGCCTTTCTCCCTTCGGGAAGCGTGGCGTTCTC ceetgeegettaceggatacetgteegeettteteeettegggaagegtggegetttete AATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT 961 tgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagt GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA AGAGAGCAGTGAGGGAGAGACAGAGACTCGAATTTCCGGAGCTATTTCAGTTTTCTTTTC CGTTTTGTGCAATTTCACTTATGATACCGGCCAATGCTTGGTTGCTATTTTGGAAACTCC cgttttgtgcaatttcacttatgataccggccaatgcttggttgctattttggaaactcc CCTTAGGGGATGCCCCTCAACTGGCCCTATAAAGGGCCAGGCCTGAGCTGCAGAGGATTCC ggcctgctcccttatcgggaagcggggcgcatcatatcaaatgacgccgccgttgaaagt GITACGITGAGAAAGAATTCCTGCAGCCCGCCGTTGCTGCCGCGTTTTTCCATAGGCTCC 541 agatitagagtetgeteeetttggeegetegggaaeeeeaeeagggtaatgettttaet GGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGCCGCTGTAAAGT TGCAGAGGATCAAGACAGCACGTGGACCTCGCACAGCCTCTCCCACA 1547 1261 1261 1441 841 1021 1501 541 601 661 721 721 781 781 841 901 901 961 601 661 g QQ Qγ g δy qq δy pp QY qq QY qq QΛ qq ŏλ qq δ Pp ŏ q Qγ g Ωp qq g ÓΥ Q φ ά δŽ QΛ

AAV21733 ID AAV2

481

qq

AAV21733 standard; cDNA; 1807

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comprising human derived promoter for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 1807;
                                                                                                 Location/Qualifiers
472.580
Arage C Anote "SupF gene"
686.1292
Arage G E ColEl origin of replication"
                                                      Vector; vaccine; tumour; antigen; plasmid pITL-1; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.7%; Score 1310.4; 99.9%; Pred. No. 0;
                                                                                                                                                               /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                anised polynucleotide vectors - sequence acceptance site, used
                                                                                                                                                                                                                                                                                                                     Claim 14; Page 56; 125pp; English.
                                                                  Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                    97WO-US14306
                                                                                                                                                                                                                                  96US-0023931
                                                                                                                                                      ..1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.7
Best Local Similarity 99.9
Matches 1311; Conservative
                                                                                                                                                                                                                                                                                               Humanised polynucleotide
                                     Humanised vector pITL-1.
                                                                                                                                                                                                                                                                 Nelson PJ;
                                                                                                                                                      1605.
                                                                                                                                                                                                                                                                                NPI; 1998-159552/14.
                                                                                                                                 misc_feature
                                                                                                                                                                                                                   14-AUG-1997;
                                                                                                                                                                                      WO9806863-A1
                                                                                                                                                                                                                                  14-AUG-1996;
                      17-AUG-1998
                                                                                                                                                                                                     19-FEB-1998
                                                                                                                                                                                                                                                                 Welson EL,
                                                                                   Synthetic.
       AAV21733;
                                                                                                                                                       promoter
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polynucleotide vectors. The vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH colynucleotide vectors. The vector in Escherichia coli DH colynucleotide vectors. The vector somprise a human deralved promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site (see AAV2173-36) which accepts cDNA products from RT-PCR coloning. They also contain minimal non-human components, such as a replication origin (see AAV21715) and selectable marker gene (see AAV2171-18) that are necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response to the target sequences with little or no immune response to the target sequences with little or no immune response to the target sequences with little or no immune response to the target sequences with little or no immune response to the target sequences with little or no immune response to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expensesed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.

Sequence 1807 BP; 419 A; 463 C; 492 G; 433 T; 0 other;

1141 CTAGAAGGACAGTATTTGGTATCTGCGCTCTGAGCCAGTTACCTTCGGAAAAAGAG 1200

Qγ

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Gaps

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Indels

1;

Pred. No. 0; 0; Mismatches

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TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT 1020 tgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagt 1020 840 240 360 360 480 480 540 900 9 GCCCCCCTGACGAGCATCACAAAATGGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG 780 900 GCCATATGGTCAGTGGATGCCTTGACCCCAGGCGGGGATGGGGGGAGACCTGTAGTCAGAG 541 agatttagagtetgeteeetttggeegetegggaaceeeaceacgggtaatgettttact GTTACGTTGAGAAAGAATTCCTGCAGCCCGCGCGTTGCTGCCGCGTTTTTCCATAGGCTCC GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGA AATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACAGGATTAGCA 121 ccctggactgttgaacgaggtcggcgtagacggtctgacgacacgcaaactggcggaacg TCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCTAATAAATTAAGTT GCATCATTTTGTCTGACTAGGTGTCCTCTATAATATATAAGCTTGATATCGAATTCTTT CGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAAGTCGATGACGGC AGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGTAATGCTTTTACT GGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGCCGCTGTAAAGT GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA GTTGGGGGGTGCAGCCGGCGGTTTACTGGCACTTCAGGAACAAGCGGGCGCCTTAAGG CCCTGGACTGTTGAACGAGGTCGGCGTAGACGGTCTGACGACACGCAAACTGGCGGAACG 541 196 1021 241 301 301 361 661 781 781 961 1021 61 121 181 421 481 661 721 901 g QQ QQ ò qq δý οg δ g οy g οy Q ò g ά qq δy g QY q ò qq δ g à g à g à Db ŏ a ò οy

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                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised polynucleotide vectors – comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid pITL-1 GFP comprises base vector pITL-1 (see AAV21733) and a humanised green fluorescent protein (GFP) reporter sequence (see AAV21725). Novel humanised vectors comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which accepts cDNA products from RT-PCR cloning. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune
 1261 AGCAGCAGATTACGCGCAGAAAAAAGGATCTGGGGGATCCGGAGAGCTCAC 1312
                                                                         plasmid pITL-1 GFP;
                                                                                                                                                                                                                                                                                                                                                                  replication"
                                                                                                                                                                                                                                                                                                           /product= green fluorescent protein 973..1181
                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "RANTES promoter"
                                                                                                                                                                                                                                                                                                                                                                  origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 57-58; 125pp; English
                                                                                                                                                                                                                                                                               Location/Qualifiers
20..734
                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "SupF gene"
1191..1793
                                                                                                                                                                                                         tumour; antigen;
                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/note= "ColE1 c
2063..2308
                                                                                                                               AAV21734 standard; cDNA; 2308
                                                                                                                                                                                                                  green fluorescent protein; ds
                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
Chimeric - Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US14306
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                                                                                                                                                                                       Humanised vector pITL-1 GFP
                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nelson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-159552/14.
                                                                                                                                                                                                          Vector; vaccine;
                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                               W09806863-A1
                                                                                                                                                                    17-AUG-1998
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                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                  AAV21734
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           1141
                                              1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              759
                                                                                                                                                                                                                                                                                                                                  781 gggggagacctgtagtcagagcccccgggcagcacaggccaatgcccgtccttcccctgc 840
                                                                                                                                                                                                                                                                                                                                                                                       519
                                                                                                                                                                                                                                                              721 gtacaagtgagcgccttaagggccatatggtgagtggatgccttgaccccaggcggggat 780
                                                                                                                                                                                                                                                                                                 GGGGGAGACCTGTAGTCAGAGCCCCCGGGCAGCACAGGCCAAATGCCCGTCCTTCCCCTGC 339
                                                                                                                                                                                                                                                                                                                                                                      AGGATGAGTAGTGAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCC 399
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTTGATATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCITCGAAGTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000 CCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGTCCTAATAAAATTAAGTTGCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 ACCACGGGTAATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 AATGACGCCCCCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGC
                                                                                                                                                                                                                               220 GAACAAGCGGGCGCCTTAAGGGCCATATGGTGAGTGGATGCCTTGACCCCAGGCGGGGAT
responses to the target sequences with little or no immune respon to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately presented on antigen presenting cells.
                                                                                                                                                              2308
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                                                                                                                                                              Length
                                                                                                                                                                                                4; Indels
                                                                                                         0 other;
                                                                                                                                                              DB 19;
                                                                                                           532 T;
                                                                                                                                                            Score 1086.6;
                                                                                                                                                                              Pred. No. 0;
0; Mismatches
                                                                                                           Sequence 2308 BP; 571 A; 601 C; 604 G;
                                                                                                                                                                70.2%;
                                                                                                                                                                Query Match
Best Local Similarity 99.6
Matches 1089; Conservative
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Aruffo A,
                                                                                                                                                                                                                 WPI; 1992-056864/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen gene.
                                                                                            15-JUL-1990;
                                                                                                                          13-JUL-1990;
                                 WO9201049-A
                                                             23-JAN-1992
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Best Local S1
Matches 7889
                                                                                                                                                                                    Seed B,
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      qq
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                 'note= "remnant of ASV LTR fragment (PvuII to MIu1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancer'
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/label= supF_gene
/note= "derived from synthetic tyrosine suppressor
1120 GGTGGCCTAACTACGCCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGC
                                                            /note= "derived from HIV TATA and tat responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "derived from SV40 origin of replication"
7918..2922
/*tag= 1
                                                                                                                                                                                                                                                                                                                                                                                                                   cloning technique; CD2; cell surface antigen; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "derived from cytomegalovirus AD169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "derived from piLNXAN polylinker"
2570..2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "derived from pSV to splice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "derived from pivx, remnant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "derived from pMB1 origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'function= polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /funčtion= linker
/note= "SacII linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..589
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                                                                                                                                                                                                                                                                                          AAQ21163 standard; cDNA; 2932 BP.
                                                                                                                                                                                                                                                                                                                                                                                     COS cell expression vector piH3
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/function= ori
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/nof
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590..597
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                                                                                                                                                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This COS cell expression vector was constructed from pisv (Little et al., Mol. Biol. Med. 1:473-488 (1983)) by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. The transcription unit consisted of a chimeric promoter composed of human cytomegalovirus AD169 immediate early enhancer sequences fused to the HIV LTR -67 to (plus)80 sequences. A polylinker contg. 2 BstXI sites separated by a 350bp stuffer was inserted immediately downstream from the LTR (plus)80 sequence. Downstream from the polylinker were placed the SV40 small tantigen splice and early region polyadenylation signals derived from pSV2. The new vector, which forms part of the wider disclosure of the specification, was used in the cloning of the human CD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                          New CD53 cell surface antigen and DNA encoding it - for immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2932 BP; 775 A; 698 C; 682 G; 777 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 755; DB 13;
Pred. No. 3.9e-219;
0; Mismatches 15;
poly-A addition signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 160pp; English.
                                                                                                                                                                                                                                                                                            Amiot M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 48.8%;
Local Similarity 97.6%;
es 788; Conservative
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     1008
                                                      ACAGGATTAGCAGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA 1128
                                                                               ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                         TCGGAAAAAGGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT 1248
                                                             949 AGCTGGGCTGTGTGCACGAACCCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACT
         1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACCACGGTA
                                   /function= synthetic tyrosine suppressor tRNA gene 800..947
                                                                                                                                                                                                                                 CD19; cell surface antigen; T lymphocyte; immunoselection cloning; vector; piH3; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                           elements
                                                                                                                                                                                                                                                                                                                                                                                                                               /function= pSV splice and poly-Addition signals 2570..2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function= SV40 origin of replication (PvuII to HindIII
                                                                                                                                                                                                                                                                Location/Qualifiers
1..589
/*tag= a
/note= "bases derived from pMB1 origin (pBR322
                                                                                                                                                                                                                                                                                                                                                                        enhancer
                                                                                                                                                                                                                                                                                                                                                  /function= ASV LTR fragment (PvuII to MluI) 948..1500
                                                                                                                                                                                                                                                                                                                                                                      /function= human cytomegalovirus AD169
1501..1650
                                                                                                                                                                                                                                                                                                                                                                                        /function= HIV TATA and tat-responsive
1651..1761
                                                                                                                                                                                                                                                                                                                                                                                                             /function= piLNXAN polylinker (HindIII 1717..2569
                                                                                                                                                                                                                                                                                                       /*tag= b
/function= SacI linker
598..799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             804 AGCAGATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 CCGCTGTAAAGIGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGC 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector piH3 (AAT38557), deposited as ATCC 67634, can be used in a novel immunoselection cloning method for cell surface antigen genes, e.g. human CD19 (see also AAT38556). This involves introducing CDNA fragments into the vector, transfecting mammalian cells in culture, maintaining the cells under conditions that allow antigen expression, exposing the cells to an antibody directed against the antigen, and recovering positive cells by contact with an immobilised antibody directed against the first antibody.
/function= piVX, remnant of R1 site from polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 GTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           769 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCCTGGAAGCTCCCTCGTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
                                                                                                                                                                                                                                                                                                                                                                               encoding CD19 cell surface antigen - useful for recombinant fen prodn. for diagnostic and therapeutic purposes
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                                                                                                                                                                                                                                                                       Camerini D, Lauffer L, Oquendo C; Stamenkovic I, Stengelin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2932 BP; 773 A; 700 C; 682 G; 777 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 755; DB 17;
Pred. No. 3.9e-219;
0; Mismatches 15;
                                                                                                                                                                                                                         (MASS-) MASSACHUSETTS GEN HOSPITAL.
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                                                                                                                                   89EP-0103127
                                                                                                                                                                               88US-0160416
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Best Local Similarity 97.67
Matches 788; Conservative
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Simmons D,
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                                                                                                                                                                                                                                                                                                                                                                                                             antigen prodn.
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                                                                                                                                                                               25-FEB-1988;
                                              EP739980-A2
                                                                                       30-0CT-1996
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                                                        ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTA 1068
                               ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCGTA 1128
                                                                                   /note- "bases 1501-1650 are derived from HIV TATA
                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "bases 800-947 are derived from a remnant
of the ASV LTR fragment (PvuII-MluI)"
                                                                                                                                                                                                                                                                                                                                                                                              /note= "bases 948-1500 are derived from the hCMV AD169 enhancer"
                                                                                                                                                                                                                 Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; dlagnosis; vector; piH3; CD2; T-cell receptor; COS;
                                                                                                                                                                                                                                                                             /note= "bases 1-589 are derived from the pMB1 ____origin (pBR322 ori)"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= g /*tag= g //note= "bases 1651-1716 are derived from the piLNXAN polylinker (HindIII-Xba)" 1717...2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "bases 1717-2569 are derived from psv
to splice and poly-Addition signals"
2570..2917
                                                                                                                                                                                                                                                                                                                            /*tag= c /note= "bases 598-799 are derived from the synthetic tyrosine suppressor tRNA gene (supF gene)"
                                                                                                                                                                                                                                                                                                 /*tag= b
/note= "bases 590-597 are derived from
SacII linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                 and tat-responsive elements"
                                                                                                                                                                                                                                                          Location/Qualifiers
1..589
                                                                                                                     AAT14702 standard; DNA; 2932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector piH3 (AAT14702) is a COS cell expression vector constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. This novel vector allows the generation of very large mammalian expression libraries and yields large amounts of protein in mammalian host cells, resulting in efficient selection. Efficiency of library construction is comparable to that achieved with phage lambda, but the clones generated are easier to manipulate. A novel immunoselection cloning method was used to clone genes (see also AAT14703-04 and AAT14706-26) for cell surface antigens of human lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624 CCGCTGTAAAGTGTTACGTTGAGAAAGA---CCGCGGTAATTCGGCGTTGCTGGCGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC
/*tag= i
/note= "bases 2570-2917 are derived from the SV40
origin of replication (PvuII-HindIII)"
2918..2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
                                                                                                 /*tag= j
/note= "bases 2918-2922 are derived from pivX,
remnant of R1 site from polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2932 BP; 774 A; 698 C; 683 G; 777 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%; Score 755; DB 17;
97.6%; Pred. No. 3.9e-219;
tive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1A-B; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                           88US-0160416.
89US-0379076.
90US-0553759.
93US-0139273.
                                                                                                                                                                                                                                                                                                    88US-0160416
                                                                                                                                                                                                                                                                                                                                                      92US-0983647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.6
Matches 788; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-200279/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aruffo A, Seed B;
                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
18-OCT-1993;
                                                                                                                                                                                                                                                                                                    25-FEB-1988;
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                                                          1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTA 1068
        CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG 888
                                                                                                                                                                    89
                                                                                                                                                                                                   29
                            TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
                                     1069 ACAGGATTAGCAGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
                                                                                                                                                            1129 ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "from synthetic tyrosine suppressor tRNA
                                                                                                                                                                                                                                                                                                                               Vector; piH3; cell surface antigen; lymphocyte; human; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/note= "human cytomegalovirus AD169 enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **tag= f
'note= "HIV TATA and tat-responsive elements"
                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "from pMbl origin (pBR322 ori)"
590..597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
/note= "ASV LTR fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dene (supF dene)
                                                                                                                                                                                                                                                                                                                                                           - Human cytomegalovirus.
Human immunodeficiency virus.
- Rhesus macaque polyoma virus.
                                                                                                                                                                                                                TTTTTGTTTGCAAGCAGCAGATTACGC 1275
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "SalI linker"
598..799
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..589
                                                                                                                                                                                                                       AAV63441 standard; DNA; 2932
                                                                                                                                                                                                                                                                                                                                                     Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                07-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501..1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1651..1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800..947
                                                                                                                                                                                                                                                                                                                Expression vector piH3
                                                                                                                                                                                                                                                                                                                                                                                          Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                            Chimeric
Chimeric
                                                                                                                                                                                                                                                                                   AAV63441;
                                                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhancer
                                                                                                                                                                                                                                                                                                                                      cos; ss
                                                                                                                                                                                                                                                    RESULT 7
AAV6341/C
ID AAV634
XX
AC AAV634
XX
XX
DE Express
XX
XX
Chimer
OS Chimer
OS Chimer
OS Chimer
CS Chimer
FT misc_f
FT misc_f
FT misc_f
FT TATA_S
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829
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This is the nucleotide sequence of expression vector piH3, a COS cell expression vector constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SY40 origin. The vector can be used in a novel method for cloning cDNAs from mammalian expression libraries. The method is cloning cDNAs from mammalian expression libraries. The method is immunoselection of cells expression of an antigen in eukaryotic cells and inmunoselection of cells expression of an antibody-coated substrate. The method is useful for the can antibody-coated substrate. The method is useful for the capressed and transported to the cell surface membrane of a cukaryotic cell. It has been used to clone genes encoding cell surface antigens associated with mammalian T lymphocyte antigens such as CDI-53. IRA-3, ICAM-1, FRI, TLISA and Leuß (see AAV63442-63 and AAW80440-55). The invention provides high efficiency expression vectors, such as piH3, which allow the generation of very large mammalian expression libraries, and yield large amounts of protein in mammalian host cells, resulting in efficient selection. The purified genes and proteins are useful for immunodiagnostic and immunocherapeutic applications, including the diagnostic and immunocherapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cloning vector and polylinker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune-mediated infections, diseases, and disorders of
                                                                    /..oue= "SV40 small t antigen splice and early region polyA signals from pSV2" 2570..2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2932;
                                                                                                                                                                                                                                                                                   /*tag- j
/note= "from pivX, remnant of R1 site from
polylinker"
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                                                                                                                                                                                           /*tag= i
/note= "SV40 origin of replication"
2918..2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%; Score 755; DB 19;
llarity 97.6%; Pred. No. 3.9e-219;
Conservative 0; Mismatches 15;
"piLNXAN polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human lymphocyte antigenic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1A-B; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88US-0160416.
89US-0379076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0861205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0983647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0861205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP.
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                                                             /*tag=
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seed B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 788; Conserv
                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    US5830731-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1988;
13-JUL-1989;
                              misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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/\*tag=

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Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;
                                                    enhancer
1068
                                                                                                                                                                                                                         ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                                                                                                                                                                AGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGGCCTTATCCGGTAACT 1008
                                                                                                                                                                                                 ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA 1128
                                                                                                                                                                                948
                                                                                                                                 8
                                                                                                                                                                                                                                                            29
    1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTA
                                                                                                                                                                                                                                                      CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
                                                                                                                          TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
                                                                                                                                                                                                                               CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT
                                                  TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC
                                                                           GAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                CD40; cell surface antigen; human; vector; plasmid piH3;
cDNA library; COS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..589
/*tag= a
/note= "from pMB1 origin (pBR322 ori)"
590..597
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Escherichia coli.
Chimeric - Human cytomegalovirus.
Chimeric - Human immunodeficiency virus.
Chimeric - Rhesus macaque polyoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                  - Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                       AAV81199 standard; DNA; 2932
                                                                                                                                                                                                                                                                                                                                        10-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Expression vector piH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                            AAV81199;
                                                                                                                                                                                                                                                                                                          CD40;
                684
                                                                                      507
                                                                                                                                                  949
                                                                                                                                                                                     267
                                                                                                                                                                                                            207
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                                                                                                             447
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    589
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This is the nucleotide sequence of expression vector piH3, a COS cell expression vector constructed from piSV by inserting a cell expression vector constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. The vector can be used in a novel method for cloning cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate, such as a culture dish. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. The invention specifically provides the CD40 c DNA sequence (see AAV81198). It also provides high efficiency expression vectors, such as pH3, which allow the generation of very large mammalian expression libraries, and yield large amounts of protein in mammalian host cells, resulting in efficient selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expression vectors for expression in eukaryotic cells or their fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "pivx, remnant of R1 site from polylinker"
                                                                             /*tag= c
/note= "from synthetic tyrosine suppressor tRNA
gene (supF gene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /HOUCE "SV40 small t antigen splice and early region polyA signals from pSV2" 2570..2917
                                                                                                                                                                                                                                                                                                                                                                 /note= "HIV TATA and tat-responsive elements"
                                                                                                                                                                                                                                                              /*tag= e
/note= "human cytomegalovirus AD169 enhancer"
1501..1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Camerini D, Lauffer L;
, Stamenkovic I, Stengelin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= i
/note= "SV40 origin of replication"
2918..2922
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/note= "piLNXAN polylinker"
                                                                                                                                                                                /*tag= d
/note= "ASV LTR fragment"
b
"Sall linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1A-B; 79pp; English.
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Simmons D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0983647.
88US-0160416.
89US-0379076.
90US-0498809.
90US-0553759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "piI
1717..2569
                                                                                                                                                                                                                                                                                                                                                                                         1651..1716
                                                                                                                                                                                                                                948..1500
/*tag= e
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                             /note= "S:
598..799
/*tag= c
                                                                                                                                                        800..947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amiot M,
                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1990;
13-JUL-1990;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                   TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_signal
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Oquendo C,
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5
                                         AGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACT 1008
                                                                                                                                                                                                                                                                                                                              1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTA 1068
                               469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                      648
                                                                                                         Gaps
                                                                                                                                      708
                                                                                                                                                      568
                                                                                                                                                                TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC 768
                                                                                                                                                                                                                                                                                                                                                               1069 ACAGGATTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCGTA 1128
                                                                                                                                                                                                                                                                                                                                                                                               ACTACGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGGTGAAGCCAGTTACCT 1188
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                                                                                                                                                                                                                                                                        AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGGCGCATCATATCAAATGACGCG
                                                                                                                               CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT
                                                                                                                                         GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT
                                                                                                                                                                                                         CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
                                                                                                                                                                                                                                                               889 IGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
     Length 2932;
                    Indels
/ Match 48.8%; Score 755; DB 20; Local Similarity 97.6%; Pred. No. 3.9e-219; nes 788; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
AAA50577/c
ID AAA50577 standard; DNA; 2932 BP
XX
AC AAA50577;
XX
DT 19-DEC-2000 (first entry)
XX
XX
XX
XX
XX
KW Plasmid piH3; vector; eukaryotis
 Query Match
               Matches
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                                                                                                               684
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Plasmid piH3; vector; eukaryotic cell; COS; cell surface antigen;

Eukaryotic cell expression vector plasmid piH3.

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Isolated nucleic acid molecule encoding the CDI9 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                       to splice and poly-A site"
                                                                                                                                                                                                                                     note= "synthetic tyrosine suppressor tRNA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of COS cell expression vector plasmid piH3. The vector was constructed from piSV by inserting
                                                                                                                                                                                                                                                                                            **tag= e
'note= "human cytomegalovirus AD169 enhancer"
                                                                                                                                                                                                                                                                                                                1501..1650
/*tag= f
/note= "HIV TATA and tat-responsive element"
                 complex disease;
immunodiagnosis; diagnosis; immunotherapy; gene therapy;
immune disorder; infection; asthma; immune-complex disea.
amyloidosis; multiple sclerosis; parasitic disease;
immunoselection; panning; ds.
                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/note= "derived from piLNXAN polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                //fuction= "replication origin"
/note= "from SV40 origin of replication"
2918..2922
                                                                                                                                                                                                                                                            /*tag= d
/note= "remnant of ASV LTR fragment"
                                                                                                                                                                                   /*tag= b
/note= "derived from SacI linker"
                                                                                                                                                       origin"
pMB1"
                                                                                                                                                                                                                                                                                                                                                                            1717..2569
/*tag= h
/note= "derived from psv
                                                  Chimeric - Rhesus macaque polyoma virus.
Chimeric - Escherichia coli.
Chimeric - Human cytomegalovirus.
Chimeric - Human immunodeficiency virus.
Chimeric - Synthetic.
                                                                                                                                             /function= "replication
/note= "pBR322 ori from
590..597
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "from pivx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1A-B; 75pp; English.
                                                                                                                                                                                                                  /*tag= c
/gene= "supF"
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88US-0160416.
89US-0379076.
90US-0498809.
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/*tag= i
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                                                                                                                                1..589
/*tag=
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                                                                                                                             misc_feature
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25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
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                                                                                                                                                                                                                                                                                                               TATA_signal
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the Syd Origin. The transcription unit between the suppressor tRNA gene and the Syd Origin. The transcription unit consisted of a chimeric promoter composed of human cytomegalovirus ADIG6 immediate early enhancer sequences fused to the HIV LTR -67 to +80 sequences.

Immediately downstream from the LTR +80 was inserted a polylinker containing 2 BSKIX itses separated by a 350 bp stuffer. The BSKIX sites were flanked by Xbal sites, which could also be used to excise the insert. Downstream from the polylinker were placed the Syd 0 small t antigen splice and early region polyh signals derived from pSV2. The vector can be used to construct large mammalian cDNA expression libraries. A new method for cloning cDNA encoding cONA expression libraries. A new method for cloning cDNA enciding the antigen by adhesion to (panning on) an antibody expressing the antigen by adhesion to (panning on) an antibody coated substrate such as a culture dish. The purified cDNA and immunotherapeutic applications, including the diagnosis and immunotherapeutic applications, including the diagnosis and immunor-complex disease, amyloidosis, parasitic diseases or multiple scherolist in the invention, including large amounts of protein in mammalian host cells, resulting in efficient selection.
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Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA 1068
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                          Gaps
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                                                                                             GTCGATGACGCCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACGGGT
                                                                                                                                                                                           CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTT
                                                                                                                                                                                                                                        TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC
                                                                                                                                                                                                                                                                                                  AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCCATCATATCAAATGACGCG
                                                                                                                                                        CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
                                                                                                                                                                                                               CCGCTGTAAAGTGTTACGTTGAGAAAGA---CCGCGGTAATTCGGCGTTGCTGGCGTTTT
                                                                                                                                                                                                                                                                567 TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGC
                                                                                                                                                                                                                                                                                      GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT
                          4;
48.8%; Score 755; DB 21; Length 2932; 97.6%; Pred. No. 3.9e-219;
                       Indels
                        15;
                       0; Mismatches
                       788; Conservative
            Similarity
 Query Match
             Best Local
Matches 78
                                                                                           529
                                                                                                                   744
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Human; lymphocyte cell surface antigen; immune-mediated disease; asthma; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus erythematosus; platelet disorder; rheumatoid arthritis; transplant rejection; cyclic; circular; mutant; pill3; ds.
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                                                                        Expression vector piH3 DNA used to express human lymphocyte antigens.
                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /"cay" ...
/note= "Derived from the HIV TATA and tat-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "Derived from the synthetic tRNA gene (supF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Derived from the SV40 origin of replication
  (PvuII to HindIII)"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1.1589
7.4109 a
/note= Derived from the pMB1 origin (pBR322 ori)"
                                                                                     ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT
                                         /*tag= b
/note= "Derived from the SacII linker (ACCGCGT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/note= "Derived from the human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment (PvuII to MluI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pitnxan polylinker
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/note= "Derived from the
/HindIII to Xba)"
                                                                                                                                                                                                                                                                                                                                     - Avian sarcoma virus.
- Human cytomegalovirus.
- Human immunodeficiency virus.
- Rhesus macaque polyoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD169 enhancer"
                                                                                                                   1249 TITITGTITGCAAGCAGCAGATTACGC 1275
                                                                                                                               28 TITITIGETAGCAGCAGATTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elements"
1651..1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signals"
2570..2917
                                                                                                                                                                                              ВЪ
                                                                                                                                                                                             AAS03171 standard; DNA; 2932
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                                                                                                                                                                                                                                                                                                                                                          Chimeric -
Chimeric -
Synthetic.
                                                                                                                                                                                                                   AAS03171;
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The present sequence for expression vector piH3 is used to provide
high level expression of human lymphocyte cell surface antigens in
eukaryotic host cells. Another expression vector piH3M (AASO3174)
is also described. Various human lymphocyte cell surface antigen cDNA
sequences (AASO3172, AASO3173, AASO3195) are described
celating to the invention of a novel method of cloning cDNA
celating to the invention of a novel method of cloning cDNA
inbraries. A genetically engineered CDNA sequence encoding the CD28
amino acid extracellular domain sequence (amino acids 1-134 given in
AAUO1437) and/or comprising nucleotides 100-759, 154-555 or 154-759 of
the CD28 cDNA sequence (AASO3175) is also new. The purified genes and
proteins are useful for immunodiagnostic and immunocherapeutic
control of the control of disorders in animals and humans. Such diseases
include immune deficiency diseases, diseases of immediate type of
include immune deficiency diseases, diseases of immediate type of
the CD28 cDNA sequence (AASO3175) is also new. The control of inflammation,
control of immune deficiency diseases, diseases of immediate type of
the control of disorders in animals and humans. Such diseases
include immune deficiency diseases, diseases of immediate type of
the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA encoding CD28 useful for diagnosing and treating immune-mediated diseases, infections or disorders, e.g. systemic lupus erythematosus, asthma, transplant rejection, rheumatoid arthritis -
/note= "Derived from pivX, remnant of R1 site from
   polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and purify other antibodies and antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1A-1B; 72pp; English.
                                                                                                                                                                                                                                                         88US-0160416.
89US-0379076.
90US-0553759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Aruffo A,
                                                                                                                                                                                                                                                      25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
                                                                                                                                                                                                      01-DEC-1992;
                                                                                    US6218525-B1
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                                                       GTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGT 588
                                           469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                                                                                                                                    TCCATAGGCTCCGCCCCCCGACCAGCATCACAAAATCGACGCTCAAGTCGAGGGTGGC 768
                                                                                                              685
                                                                                                                                 AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGGCGCATCATATCAAATGACGCG 648
                                                                                                                                                                           CCGCTGTAAAGTGTTACGTTGAGAAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT 708
                         Gaps
                                                                                                  4;
  Length 2932;
                         15; Indels
 Score 755; DB 22;
Pred. No. 3.9e-219;
0; Mismatches 15;
Query Match 48.8%;
Best Local Similarity 97.6%;
Matches 788; Conservative
 Query Match
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Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;

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1068
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                                                                                                                                                                                                                                                                     TCGGAAAAAGAGTIGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT 1248
                                                                                                                AGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACT 1008
            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retroviral vector; non-primate; lentivirus; gag gene; tat gene; LTR; long terminal repeat; gene therapy; Equine infectious anemia virus; EIAV; HIV infection; MLV; ss.
 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCT
                                                 CICCIGITCCGACCCIGCCGCTTACCGGATACCIGICCGCCTTTCTCCCTTCGGGAAGCG
                                                                          889 TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
                                                                                     ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCCTCTGCTGAAGCCAGTTACCT
                                                                                                                                                                                                                                                                               ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTA
                                                                                                                                                                                           ACAGGATTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
                                                                                                                                                                                                                                          Retroviral vectors derived from a non-primate lentivirus genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitrophanous K;
                                                                                                                                                                                                                                                                                                          TTTTTGTTTGCAAGCAGCAGATTACGC 1275
                                                                                                                                                                                                                                                                                                                     Kingsman AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Fig 37; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                           AAX86928 standard; DNA; 7252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0011037.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete sequence of pSC65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-418936/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carroll MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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RESULT

lentivirus genome. These vectors comprise a deleted gag gene. The deletion in gag removes one or more nucleotides downstream of nucleotide from the non-primate lentivirus genome or lack the tat gene but includes from the non-primate lentivirus genome or lack the tat gene but includes the leader sequences between the end of the 5' long terminal repeat (LTR) and the ATG of gag. The vectors, particles or cells transfected with either of these, are useful for the delivery of nucleotides of interest to a target site (i.e. gene therapy). The retroviral vector can be used as a delivery system. Alternatively, a non-retroviral expression vector, adenovirus or plasmid can be used as a delivery system for the retroviral wectors are capable of transferring genetic material to non-dividing or slowly dividing cells. Deletion of larger regions of the gag gene in Equine infectious anemia virus (EIAN) vectors is advantageous and leads to higher titers of viral vector being produced. Deletion of accessory genes permits vectors to be produced without the genes normally associated with disease in lentiviral (e.g. HIV) infections. The deletion of these genes also permits the vector to invention provides retroviral vectors derived from a non-primate package more heterologous DNA. 

Sequence 7252 BP; 1942 A; 1686 C; 1751 G; 1873 T; 0 other

. 0 5361 5421 5481 5601 5661 5301 1080 AGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC 1139 899 660 TGTTACGTTGAGAAATTCCTGCAGCCCGCGCGTTGCTGGCGTTTTTCCATAGGCTC 719 720 CGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA 779 Gaps 5362 gigcacgaaccccccgitcagcccgaccgctgcccttaiccggtaactaicgititgag tccaacccggtaagacacgacttatcgccactggcagccactggtaacaggattagc 1140 ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGA actagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaaga ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTTCGGGAAGCGTGGCGCTTTCT GTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG 1020 TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC Length 7252; ö 16; Indels Score 607.4; DB 20; Pred. No. 5e-174; 0; Mismatches 1260 AAGCAGCAGATTACGCGCAGAAAAAAAGGATCT 1292 39.3%; 97.5%; Matches 617; Conservative Best Local Similarity Query Match 840 7 5062 5122 780 5182 096 5422 5542 1200 5602 g δ g δ QQ ŏ QQ ò qq δ g ò g ŏ g οý g ά g δ

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This sequence represents the recombinant expression plasmid FBdelPASAF.

This sequence is a packaging-deficient construct having a viral env gene (in this case from RDI14) and a selectable matrem (8M). It is an example of a recombinant expression vector (REV) of the invention, used to create a packaging cell line. The REVS of the invention comprise a gene of the second and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated stop codon is spaced from a start codon of the COI and a GOI associated suppressed as a result of the cut and series of the cell lines are replication. The cell lines are transformed with two REVS, both are replication deficient, one contains the viral gene, high titre retroviral vectors may be obtained. The packaging cell lines are useful for gene therapy. Prior packaging cell lines are useful for gene therapy. Prior packaging cell ince useful for gene therapy. Prior packaging cell solated by cotransfecting them with plasmids encoding selectable markers. However, the helper functions can be lost during the passages of the cells in culture and the current packaging systems provide limited titres of infectious retroviral vectors. Co-transfection with a plasmid encoding a SM does not directly select the best gag-pol-env-expressing cells. The new retroviral packaging cell lines overcome these problems.
                                                                                                                                                                                                      Packaging-deficient construct; viral gag-pol gene; packaging cell line; moloney murine leukaemia virus; MOMLV; viral env gene; helper construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3752 ttatcatgtctggatccagatctgggcccatgcggccgcggatcgatnnnnacatgtgag 3811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5865 BP; 1492 A; 1602 C; 1390 G; 1373 T; 8 other;
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91.4%; Pred. No. 3.7e-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takeuchi Y, Weiss RA;
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                                                                                                                                                           Plasmid FBdelPRDSAF coding sequence
                     AAT90692 standard; DNA; 5865 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB02061
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                                                                                                               (first entry)
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Best Local Similarity 91.4'
Matches 638; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins MKL, Cosset F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-179287/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CANC-) CANCER
                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re-initiation
                                                                                                                                                                                                                                                                                                                                              WO9708330-A1
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                                                                                                               05-JAN-1998
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                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                   AAT90692;
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                                                                                                                                                                                                                                                      GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 1194
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GGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
                                     775 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG
                                                                                                                    TITCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG
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ig-deficient construct; viral gag-pol gene; packaging cell line;
murine leukaemia virus; MoMLV; viral env gene; helper construct;
                                                                 Packaging-deficient construct; viral
                                                   Plasmid FBdelPASAF coding sequence.
       AAT90689 standard; DNA; 6028
                                                                                gene therapy; ss.
                                    05-JAN-1998
                                                                                               Synthetic.
                      AAT90689
                                                                         moloney
AAT90689
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RES CAMPAIGN TECHNOLOGY. 96WO-GB02061 95GB-0017263 (CANC-) CANCER 23-AUG-1996; 23-AUG-1995; WO9708330-A1 06-MAR-1997

Weiss Takeuchi Y, Cosset F, WPI; 1997-179287/16 Collins MKL,

Selectable retroviral packaging cell lines and expression constructs

TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG

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1135 GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 1194

- comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation re-initiation

Claim 13; Fig 9; 79pp; English.

This sequence is a packaging-deficient construct having a viral envolutions.

This sequence is a packaging-deficient construct having a viral env gene care (in this case from the moloney murine leukaemia virus) and a selectable marker (SM). It is an example of a recombinant expression vector (REV) of the invention comprise a gene of interest (GDI) and a SM gene. The REVS of the invention comprise a gene of interest (GDI) and a SM gene. The SM gene is arranged downstream of the GOI and a GOI associated stop codon is spaced from a start codon of the SM gene to ensure that the SM protein is expressed as a result of translation reinitiation. The cell lines are transformed with two REVs, both are replication deficient, one contains the viral gag-pol gene, the other the viral env gene. By using helper constructs, such as the REV's, which are directly selectable and which provide for high expression of the viral gene, high titre retroviral constructs may be obtained. The packaging cell lines are useful for gene therapy. Prior packaging cell lines using full length retroviral genomes as helper genomes were isolated by cotransfecting them with plasmids curing the passages of the cells in culture and the current packaging systems provide limited titres of infectious retroviral vectors.

Co-transfection with a plasmid encoding a SM does not directly select the best gady pol-env. expressing cells. The new retroviral packaging cell incentive. This sequence represents the recombinant expression plasmid FBdelPASAF lines overcome these problems. 

Sequence 6028 BP; 1515 A; 1637 C; 1499 G; 1369 T; 8 other;

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                                                                                                                                                                                                                                                                                                                                                                                           TITCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG
     Length 6028;
                                    ó;
 Score 604.4; DB 18;
Pred. No. 3.7e-173;
                                  60;
                                  0; Mismatches
Query Match 39.1%;
Best Local Similarity 91.4%;
Matches 638; Conservative
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This sequence is a packaging-deficient construct having a viral env gene
(in this case from the molonowy murine leukaemia virus) and a selectable
marker (SM). It is an example of a recombinant expression vector (REV) of
the invention, used to create a packaging cell line. The REVs of the
invention comprise a gene of interest (GOI) and a SM gene. The SM gene is
arranged downstream of the GOI and a GOI associated stop codon is spaced
from a start codon of the SM gene to ensure that the SM protein is
c expressed as a result of translation reinitiation. The cell lines are
transformed with two REVs, both are replication deficient, one contains
the viral gag-pol gene, the other the viral env gene. By using helper
constructs, such as the REVs's, which are directly selectable and which
provide for high expression of the viral gene, high titre retroviral
vectors may be obtained. The packaging cell lines are useful for gene
therapy. Prior packaging cell lines using full length retroviral
encoding selectable markers. However, the helper functions can be lost
current as a season of the cells in culture and the current packaging
curring the passages of the cells in culture and the current packaging
                                                                                                                                                                                                                                                                                                                                               Packaging-deficient construct; viral gag-pol gene; packaging cell line; moloney murine leukaemia virus; MOMLV; viral env gene; helper construct;
4455 gctacactagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaa 4514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selectable retroviral packaging cell lines and expression constructs
                                              1195 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCGCCGCTGGTAGCGGTGGTTTTTTTG
                                                                             4515 aaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcggtggttttttg

    comprise selectable gene downstream of gene of interest, are
selectable due to the in-efficiency associated with translation

                                                                                                                            1255 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeuchi Y, Weiss RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                               Plasmid FBdelPMOSAF coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 10; 79pp; English.
                                                                                                                                                                                                                       AAT90690 standard; DNA; 6061
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                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re-initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKL,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9708330-A1
                                                                                                                                                                                                                                                                                  05-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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systems provide limited titres of infectious retroviral vectors.

Co-transfection with a plasmid encoding a SM does not directly select the best gag-pol-env-expressing cells. The new retroviral packaging cell

Sequence 6061 BP; 1498 A; 1665 C; 1485 G; 1405 T; 8 other;

overcome these problems.

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                                                                                                                                                                                                                                                                                                                                                                    GCTGTGTGCACGAACCCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 1014
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                                                                                                     3948 ttatcatgtctggatccagatctgggcccatgcggccgcggatcgatnnnnacatgtgag 4007
                                                                                                                                                                         4008 caaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccata 4067
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                                     Gaps
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                                                                                                                                         TAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTTCCATA
 Length 6061;
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                                    Indels
   DB 18;
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Pred. No. 3.7e-173;
0; Mismatches 60;
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39.1%;
ilarity 91.4%;
Conservative
 Query Match
Best Local Similarity
Matches 638; Conserv
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PP 06-WAR-1997.

XX 23-AUG-1996; 96W0-GB02061.

XX 23-AUG-1995; 95GB-0017263.

XX CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XI COLLINS MIL, COSSET F, Takeuchi Y, Weiss RA;

YA COMPINE Selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation re-initiation.

YX SI Selectable due to the in-efficiency associated with translation of the in-efficiency associated with translation of the in-efficiency associated with translation.

XX C C This sequence represents the recombinant expression plasmid FEdelPASAF.

This sequence represents the recombinant expression plasmid FEDELPASAF.

This sequence represents the recombinant expression plasmid FEDELPASAF.

This sequence represents as a selectable marker (5M). It is an example of a recombinant expression vector (RRY) of the invention used to create interest (GOI) and a SM gene is a rarnaged downstream of the CC of and a GOI associated stop codon is spaced from a start codon of the interest (GOI) and a SM gene is a rarnaged downstream of the cC C of and a GOI associated stop codon is spaced from a start codon of the constant on remittation. The call lines are transformed with two REVs, oth are replicated of efficient, one contains the viral gap rol gene, the viral env gene. By using helper constructs, such as the RIVEN selectable and which provide for high expression of the viral gene, high titre retroviral vectors may be obtained. The construct packaging cell lines are useful for gene therapy. Prior packaging cell lines using full length retroviral vectors may be obtained inmited the coding a SM does not directly select the best agar-pol-env-expressing cells. The new retroviral packaging cell lines constructs and percent constructs and percent coding a SM does not directly select the best agar-pol-env-expressing cells. The new retroviral packaging cell lines overcome these problems.

Sequence 6312 BP; 1575 A; 1692 C; 1561 G; 1476 T; 8 other;
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ö 4259 caaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccata 4318 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 1014 655 TAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGTTGCTGGCGTTTTTCCATA 714 GGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 774 595 TITACIGGCCIGCICCCITAICGGGAAGCGGGGCGCAICAIAICAAAIGACGCGCGCIG 654 TITCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 954 0; Gaps 835 TICCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGGCGC Ouery Match
39.1%; Score 604.4; DB 18; Length 6312;
Best Local Similarity 91.4%; Pred. No. 3.8e-173;
Matches 638; Conservative 0; Mismatches 60; Indels 0; 4319 4439 715 4499 895 955 Ωp ŏ g ò δ qq δλ qq δy QΩ δ

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GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCAAGCCAGTTACCTTCGGAA 1194
                                                                                                                                                 gctacactagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaa 4798
                                                                                                                                                                                    AAAGAGTTGGTAGCTCTTGATCCGCCAAACCACCACCGCTGGTAGCGGTGGTTTTTTG 1254
                                            TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAACAGGA
                                                                              TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG
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Search completed: January 17, 2002, 12:04:29 Job time: 17856 sec Sequence Sequence

Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 3, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 8, Appli Sequence 8, Appli

13, Appli 8, Appli 9, Appli 8, Appli 1, Appli 8, Appli

Sequence 1, Sequence 8,

Sequence:

Run on:

Searched:

Database

Result

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OTHER INFORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3611)
OTHER INFORMATION: n is any nucleotide
FEATURE:
                  PCT-USS4-14030A-9
US-07-989-847-13
US-08-469-411-13
US-07-745-382-13
US-07-921-848-13
US-08-115-680-3
US-08-115-680-3
US-08-115-372-3
US-08-165-301A-13
US-08-810-436-13
                                                                                                                   PCT US93 0824 - 3
PCT US93 0824 - 3
PCT US94 - 14179 - 13
US 08 - 232 - 463 - 9
US 09 - 075 - 019 - 8
US - 07 - 623 - 953 - 1
US - 08 - 675 - 566 - 8
            US-08-808-324-9
                                                                                                                                                                                                                                                                        Sequence 18, Application US/09011745
Patent No. 6165715
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COLIDIS, MANY KL
APPLICANT: COLIDIS, MANY KL
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIN Ver. 2.0
SEQ THARE: 5865
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LOCATION: (3800)
OTHER INFORMATION: n is any nucleotide
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LOCATION: (3612)
OTHER INFORMATION: n is an
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3613).
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US-09-011-745-8
 LOCATION:
  (without alignments)
1582.911 Million cell updates/sec
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Sequence 6, Appli
Sequence 7, Appli
Sequence 156, App
Sequence 170, App
Sequence 9, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 17, Appli
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Sequence 41, Appl
Sequence 10, Appl
Sequence 9, Appli
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                                                                                                                   US-09-242-202A-27
1547
1 GGTACCTGCCACCATGGCGC......CTCGCACAGCCTCTCCCACA 1547
                                                                         January 17, 2002, 11:54:39; Search time 221.34 Seconds
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                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-447-430A-42
US-08-447-430A-40
US-08-447-430A-41
US-08-318-837-10
US-08-362-670B-9
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 351203 seqs, 113238999 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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6012
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1325
1305
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3303
33104
3474
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                                                                                                                                Length 5865;
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                                                                                                                            Score 604.4; DB 4;
Pred. No. 6.2e-169;
0; Mismatches 60;
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; LOCATION: (3802)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-8
                                    any nucleotide
                                                                                                                            Query Match 39.1%;
Best Local Similarity 91.4%;
Matches 638; Conservative
         NAME/KEY: misc_feature
LOCATION: (3801)
OTHER INFORMATION: n is
FEATURE:
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3915 ttatcatgtctggatccagatctgggcccatgcggccgcggatcgatnnnnacatgtgag 3974
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                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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                              CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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; CCATION: (3965)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-5
TITLE OF INVENTION: Expression systems FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide
                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n is any
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Matches 638; Conservative
                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (3774)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (3775)
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LOCATION: (3776)
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LOCATION: (3777)
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LOCATION: (3962)
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LOCATION: (3963)
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LOCATION: (3964)
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OTHER INFO
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RESULT 2 US-09-011-745-5 ; Sequence 5, Application US/09011745 ; Patent No. 6165715

GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takenchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic

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                                                                                                                GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 1014
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                                                                                                                                                                              1015 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA 1074
                                                                                                                                                                                                             4335 ttgagtccaacccggtaagacacgacttatcgccactggcagcagccactggtaacagga 4394
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                                               1075 TTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG
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OTHER INFORMATION: Description of Artificial Sequence: Portion
OTHER INFORMATION: construct
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APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Taxtenchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT PELLING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
BARLIER FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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NAME/KEY: misc_feature
LOCATION: (3807)
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NAME/KEY: misc_feature
LOCATION: (3810)
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LOCATION: (3808)
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Pred. No. 6.3e-169
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Best Local Similarity 91.4%;
Matches 638; Conservative
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                                                                                                                                                        LOCATION: (3997)
OTHER INFORMATION: n is
FEATURE:
 OTHER INFORMATION: n is
                                                                                     NAME/KEY: misc_feature
LOCATION: (3996)
OTHER INFORMATION: n is
                                                         OTHER INFORMATION: n is
                           NAME/KEY: misc_feature I.OCATION: (3995)
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LOCATION: (3998)
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                                                                                                                                  1015 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACAGGA 1074
                955 GCTGTGTGCACGAACCCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC
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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 156, Application US/08276852 Patent No. 5652138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.4%; Pred. No. 6.4e-169;
Matches 638; Conservative 0; Mismatches 60; Indels 0;
                                                                                         APPLICANT: COLLINS, MARY KL
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-22
BARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1996-08-23
SAFRIER FILING DATE: 1995-08-23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
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NAME/KEY: misc_feature
LOCATION: (4249)
CTHER INFORMATION: n is any nucleotide
US-09-011-745-7
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OTHER INFORMATION: n is any nucleotide
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                                           Sequence 7, Application US/09011745
Patent No. 6165715
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NAME/KEY: misc_feature
LOCATION: (4247)
OTHER INFORMATION: n is
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LOCATION: (4060)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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LOCATION: (4248)
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GENERAL INFORMATION:
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Pred. No. 1e-168;
0; Mismatches 13; Indels
                                                              NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REERENCE/DOCKET NUMBER: 36,163
RELEPHONE-CHOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-6312
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
            APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%;
Best Local Similarity 97.9%;
Matches 612; Conservative
PRIOR APPLICATION DATA:
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7279 TAAGGGAGAGCGTCGACCTCGGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC 7220
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                                                                             HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-UUL-1994
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,163
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 97.9
Matches 612; Conservative
                                               APPLICANT: Lerner, Richa
TITLE OF INVENTION: HUMA
TITLE OF INVENTION: TO H
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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Sequence 170, Application US/08276852 Patent No. 5652138

US-08-276-852-170/c

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6799 GACAGTATTIGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG
                                               GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG
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                                                                                                                                                                       GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG
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STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos R

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL AN

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORTAGES PATENTING SISTEM: C-10.5/MS-10.5
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/0899,575
FILING DATE: 24-5UL-1997
CLASSIFICATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-5UL-1994
APPLICATION NUMBER: US/08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/05/148
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
ATTOMET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           SCR1452P
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
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nucleic acid
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MEDIUM TYPE: Floppy
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STATE: CA
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STRANDEDNESS:
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US-08-899-575-156
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                                                                                                                   Length 13254;
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Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERCIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                                                                                Indels
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                                                                                                                Score 604.2; DB 1;
Pred. No. 1e-168;
0; Mismatches 13;
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                    MOLECULE TYPE: DNA (genomic)
                                                                                                                Query Match 39.1%;
Best Local Similarity 97.9%;
Matches 612; Conservative
circular
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6799 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 6740
                                                     668 TGAGAAAGAATTCCTGCAGCCGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
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APPLICANT: Burton, Texthor F
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIE
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEO 1156:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
                                                                                                                                                                 6679 GATTACGCGCAGAAAAAAGGATCT 6655
                                                                                                                                            1268 GATTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                   Sequence 156, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
CLASSIFICATION: 435
PRIOR APPLICATION: 435
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APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...urkeSSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite STREET: Mail Drop TPC8 CITY: La Jolla STREE: CA COUNTRY: CA JOLIA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
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US-08-899-575-170/c
; Sequence 170, Application US/08899575
; Patent No. 5804440
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FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTARTION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEFHONE: 619-554-6317
TELEFRONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 97.9%;
Matches 612; Conservative (
                                                                                                                                                                                                                                                                 LENGTH: 13254 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                 double
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                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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7039 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGA 6980
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                                                                                                                                                              TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL.1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nuclet acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                     Sequence 170, Application PC/TUS9508743 GENERAL INFORMATION:
    6576 GATTACGCGCAGAAAAAAAGGATCT 6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) PCT-US95-08743-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.1%;
Best Local Similarity 97.9%;
Matches 612; Conservative
                                                                                PCT-US95-08743-170/c
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                                                           TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 604.2; DB 5; Length
Pred. No. 1e-168;
0; Mismatches 13; Indels
                                                                                           NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-0UL-1994
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
Application PC/TUS9508743
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Best Local Similarity 97.9%;
Matches 612; Conservative
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                     GENERAL INFORMATION:
APPLICANT:
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    Seguence 156,
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TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the TITLE OF INVENTION: presence of arginine CORRESPONDENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSER: Partial ADD
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                                                                                                                                                                                      990 TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
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                                                                                 930 GIGIAGGICGIICGCICCAAGCIGGGCIGIGIGCACGAACCCCCCGIICAGCCCGACCGC
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATE: US/08/906,957
FILING DATE: 06-AUG-1997
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STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
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FILING DATE: 31-JAN-1995
ATTORNEY FAGENT INFORMATION:
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REGISTRATION NUMBER: 26,382
REFRENCE/DOCKET NUMBER: REF/I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-0500
INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method F
TITLE OF INVENTION: periplas
TITLE OF INVENTION:
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APPLICATION NUMBER:
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US-08-906-957-9
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APPLICANT: LEGOUX, Richard
APPLICANT: LEGOUX, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                    690 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.0%; Score 603; DB 1; L. 100.0%; Pred. No. 9.5e-169;
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REGISTRATION NUMBER: 26,382
REFENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
                                                                                                                                       6679 GATTACGCGCAGAAAAAAGGATCT 6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                        1268 GATTACGCGCAGAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08594469 Patent No. 5700665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA (genomic) US-08-594-469-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacon & Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 683-1080 INFORMATION FOR SEQ ID NO: 9 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1905 base pairs
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Best Local Similarity
Matches 603; Conserv
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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2343 TICTIGAAGIGGIGGCCIAACIACGGCTACACIAGAAGGACAGIATIIGGIAICIGCGCT 2284
          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STREET: UN VA
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100.0%; Pred. No. 1...
0; Mismatches
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PRIOR APPLICATION DATE:
APPLICATION NUMBER: US FILING DATE: 26-SEP-1995
APPLICATION NUMBER: JP 6-268119
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 733
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-941-647A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 603; Conservative
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STRANDEDNESS: single
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: MATUO, YUSHI
APPLICANT: TANASE, SUMIO
APPLICANT: FUNATSU, MASAHIKO
APPLICANT: FTO, MASHIKO
APPLICANT: FTO, MATRA
TITLE OF INVENTION: METHOD FOR PRODUCING ACTIVE HUMAN
TITLE OF INVENTION: ALANINE AMINOTRANSFERASE
                                                                                                                                                       ch 39.0%; Score 603; DB 2; La Similarity 100.0%; Pred. No. 9.5e-169; 603; Conservative 0; Mismatches 0;
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                                     TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-906-957-9
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APPLICANT: TANAKA, TOSHIO
APPLICANT: MATUO, YUSHI
APPLICANT: TANASE, SUMIO
                         1905 base pairs
          SEQUENCE CHARACTERISTICS
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                 LENGTH: 1905 TryPE: nucleic acid
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                                                                                                                                                                        Local Similarity
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US-08-941-647A-1/c
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667 TCT
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Pred. No. 1.2e-168;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,647A
FILING DATE: 30-SEP-1997
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US-09-242-202-29
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US-08-533-717-1
US-09-546-4114-56
US-09-546-4114-56
US-09-546-4114-56
US-09-546-4114-56
US-09-547-939A-48
US-09-547-939A-48
US-09-543-192-12
US-09-341-410-115-12
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2383.471 Million cell updates/sec
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/cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
/cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6010_COMB.seq:
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                         17159718 seqs, 8763200856 residues
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6/ptodata/2/pna/US6009
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                                                                                                            January 17, 2002, 15:13:31
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Maximum Match 100%
Listing first 45 summaries
                                                                              nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 2	
	ID	US-09-242-202-27	US-09-242-202A-27	US-09-242-202-28	US-09-242-202A-28	US-09-242-202-29	US-09-242-202A-29	10 000 000
		16		16	16	16	16	,
	Query Match Length DB	1547						0101
dР		100.0	100.0	84.7	84.7	70.2	70.2	
	Score	1547	1547	1310.4	1310.4	1086.6	1086.6	

Sequence 27, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 5, Appl Sequence 5, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 42, Appl

Sequence 31, 1 Sequence 40, Ag Sequence 40, 1

Sequence 48, Sequence 48, Sequence 12,

Sequence Sequence Sequence S

Sequence 56, Sequence 56, Sequence 56, Sequence 56,

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AGCAGCAGATTACGCCCAGAAAAAAGGATCTGGGGGATCCGGAGAGCTCACTCTAGATG 1320
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            GCCATATGGTGAGTGCATGCCTTGACCCCAGGCGGGATGGGGGGAGACCTGTAGTCAGAG
                                                          AGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGTAATGCTTTTACT
                                                                                                                                                                                                                                                                                                     GGCCTGCTCCCTTATCGGGAAGCGGGGGGCGCATCATATCAAATGACGCGCCGCTGTAAAGT
                                                                                                                                                                                                                                                                                                                                                     GTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGTTGCTGGCGTTTTTCCATAGGCTCC
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                                                                                             CGGACTTTTGAAAGTGATGGTGGTGGTGGGGAAGGATTCGAACCTTCGAAGTCGATGACGGC
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Sequence 86, Appl
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Sequence 10, Appl
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                                                                                                                                                              APFLICATION: Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR POLYNUCLEOTIDE VACCINES
 US-09-485-737A-86
US-09-485-737B-86
US-07-671-058-7
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                    US-09-742-373-10
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202
FILING DATE: 01-Nov-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/023931
FILING DATE: 14-NuG-196
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1547;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                 Sequence 27, Application US/09242202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1547 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                          APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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  18
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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US-09-242-202-27
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NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                      MORGAN & FINNEGAN, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202A
FILING DATE: 20-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL VECTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
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                                                                                                                                                                                                                                                                    Sequence 27, Application US/09242202A GENERAL INFORMATION:
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STREET: 345 PARK AVENUE
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                                                                                                                                                                                                                                                                                                         Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
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ZIP: 10154
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Matches 1547; Conservative

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Local Similarity

Query Match

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HYPOTHETICAL:
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GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA 1140
                    CTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG 1200
                               1501 TGCAGAGGATCAAGACAGCACGTGGACCTCGCACAGCCTCTCCCCACA 1547
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TITLE OF INVENTION: NOVEL VECTOR FOR
POLYNUCLEOTIDE VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                       L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/242,202
FILING DATE: 01-Nov-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: DISKETTE, 3.5 INCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN,
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09242202
GENERAL INFORMATION:
APPLICANT: Nelson, Edward L.
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 28:
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MOLECULE TYPE: CDNA
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                                                                                 Indels
                                                          DB 16;
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                                                         Score 1310.4;
Pred. No. 0;
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            28:
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                           84.7%;
99.9%;
                                                                     Best_Local Similarity 99.5
Matches 1311; Conservative
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Query Match
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TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT
                                        CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACAGGATTAGCA
                                                                                                                            CTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG
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                                                                                                                                                                                                                                                                                                                                         POLYNUCLEOTIDE VACCINES
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN N. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
                                                                                                                                                                                                                                                                                                                                                                        L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/242,202A FILING DATE: 20-Apr-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
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STREET: 345 PARK AVENUE
CITY: NEW YORK
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TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09242202A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                           APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
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US-09-242-202A-28
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                                     Indels
        DB 16;
Score 1310.4;
Pred. No. 0;
                                      0; Mismatches
      84.7%;
99.9%;
                    Best Local Similarity 99.9
Matches 1311; Conservative
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                     340 AGGATGAGTAGTGAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCC
                                                             GGGGGAGACCTGTAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGC
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1081 GAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACGGCTACGCTACACA
                                                                                                                          GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA
                                                                                                                                                                  Score 1086.6; DB 16; Length 2308;
Pred. No. 9.6e-310;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                       AGCAGCAGATTACGCGCAGAAAAAAAGGATCTGGGGGGATCCGGAGAGCTCAC 1312
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APPLICATION NUMBER: US/09/242,202 FILING DATE: 01-Nov-1999 PRIOR APPLICATION DATE: RELING DATE: 14-AUG-1996
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nelson, Edward L.
Nelson, Peter J.
TITLE OF INVENTION: NOVEL, VECTOR FOR
POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAS: (212) 751-6849
TELEEX: 421792
                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09242202 GENERAL INFORMATION:
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LENGTH: 2308 base pairs
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NAME: KATHRYN M. BROWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Best Local Similarity
Matches 1089; Conserv
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US-09-242-202-29
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1411 TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACGCTGCGCTGCGCCTTTT 1500
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                                                                           1021 ACCITCGAAGTCGATGAGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCC
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TITLE OF INVENTION: Retroviral Vectors
FILE REFERENCE: 674523-2006
CURRENT APPLICATION NUMBER: US/09/238,356
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: PCT/GB/03876
PRIOR FILING DATE: 1998-12-22
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09238356 GENERAL INFORMATION:
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Pred. No. 9.6e-310;
                                                                                                                                                                        Nelson, Peter J.
INVENTION: NOVEL VECTOR FOR
POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
                                                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FINNEGAN, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/242,202A FILING DATE: 20-Apr-2000 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
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TELEFAX: (212) 751-6849
                                                                                                               Sequence 29, Application US/09242202A GENERAL INFORMATION:
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LENGTH: 2308 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                      STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                    APPLICANT: Nelson, Edward L.
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INFORMATION FOR SEQ ID NO: 29:
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99.6%;
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                                                                                                                                                                                                                                                                                                                             STATE: NEW YORK
1801 CCGGAGAGCTCCC 1813
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Best Local 5
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NUMBER OF SEQUENCES:
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FEATURE:
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US-08-480-120-15
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GENERAL INFORMATION:
APPLICANT: Joliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Pullto, Virginia L.
TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
                                                                                                                                                                                                              16; Indels
                                                                                                                                                                               Query Match
39.3%; Score 607.4; DB 16;
Best Local Similarity 97.5%; Pred. No. 8.5e-168;
Matches 617; Conservative 0; Mismatches 16;
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ORGANISM: Artificial Sequence, plasmid
                                          FEATURE:

NAME/KEY: misc_feature

LOCATION: (1):.(7252)

OTHER INFORMATION: plasmid vector

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AX003206

DATABASE BATRY DATE: 2000-08-24

RELEVANT RESIDUES: (1):.(7252)
SEQ ID NO 27
LENGTH: 7252
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                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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39.1%; Score 604.2; DB 8;
Best Local Similarity 97.9%; Pred. No. 7.4e-167;
Matches 612; Conservative 0; Mismatches 13;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/480,120
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT NOT 330

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9598

TELEPOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELERX: (516) 742-4366

TELEX: 30 901 SANS UR

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 7073 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                              United States
                                                                                                           ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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1268..1594
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MOLECULE TYPE: peptide
FEATURE:
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LOCATION: 1111..1146
FEATURE:
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                                      STREET: 400 Garder
CITY: Garden City
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                                                                               New York
                                                                        STATE: New COUNTRY: Un ZIP: 11530
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LOCATION: 6
FEATURE:
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CORRESPONDENCE ADDRESS
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3156 ACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC 3215
                             1028 GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG 1087
                                                                                      1088 GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACATAGAAG 1147
                                                                                                       3276 GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACAGAGAG 3335
                                                                                                                                                                                                         Gaps
                                                                                                                                                 1148 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG
                                                                                                                                                                           3336 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08480120
GENERAL INFORMATION:
APPLICANT: JOLIÉE, Linda K.
APPLICANT: JOLIÉE, Linda K.
APPLICANT: PULICO, VITGÍNIA L.
TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 604.2; DB 8;
Pred. No. 7.7e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: US/08/480,120 CLASSIFICATION: 530 TORNEY/ADDATE:
                                                                                                                                                                                                                                                                                    1268 GAFTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DiG1glio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.1
Best Local Similarity 97.9
Matches 612; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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STATE: New York
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; LOCATION:
US-08-480-120-20
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1735 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 1794
                            1495 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGA 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    847
                                                                                                                                                                                               AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCC
                                                                                                                                                                                                                      1375 AAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGCTCCGACCTGCCCTGCC
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TGAGAAAGAATTCCTGCAGCCCGCCGTTGCTGGCGTTTTTTCCATAGGCTCCGCCCCC
                                                                                                 TGACGACCATCACAAAAATCGACGCTCAAGTCAGGTGGCGAAAACCCGACAGGACTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.44
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APPLICATION NUMBER: US/09/242,202
FILING DATE: 01-Nov-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH,
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
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APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 345 PARK AVENUE CITY: NEW YORK
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GENERAL INFORMATION:
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        NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAR: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                               LENGIH: 608 base pairs
ATTORNEY/AGENT INFORMATION:
                                                                                                                             TYPE: nucleic acià
STRANDEDNESS: single
                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                     Matches 603; Conservative
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Best Local Similarity
                                                                                                                                                                                       ANTI-SENSE: NO
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US-09-242-202A-26; Sequence 26, Application US/09242202A

RESULT 11

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TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCGAACCCGGTAAGACACGACTTATCGCCA 1049
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100.0%; Pred. No. 6e-167;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                        MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: AGHERYN M. BROWN
RECIETRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202A
PILIOR DATE: 20-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
                 Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR
                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-242-202A-26
                                                         POLYNUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
                                                                                                                          STREET: 345 PARK AVENUE CITY: NEW YORK
APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
                                                                        SEQUENCES: 29
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                 STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 603; Conservative
                                                                                                                                                                                    COUNTRY: USA
ZIP: 10154
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1050 CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG 1109
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                                                                       ACCGCTGGTAGCGGTGTTTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGA
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                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09496445
GENERAL INFORMATION:
APPLICANT: MCNelsh, John D.
APPLICANT: Ahlijnian, Michael K
TITLE OF INFORTION: Transgenic Animals Expressing Human FILE REFERENCE: PC10142A
CURRENT APPLICATION NUMBER: US/09/496,445
CURRENT FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.0%; Score 603; 22.0.1.10.16; 100.0%; Pred. No. 1.1e-166; tive 0; Mismatches 0;
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Matches 603; Conservative
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ORGANISM: Escherichia
US-09-496-445-5
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                                                                                    1857
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               366 CTGGCAGCAGCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG
                                                                                                                                    486 CIGCIGAAGCCAGITACCTICGGAAAAAGAGTIGGTAGCICTIGAICCGCCAAACAAACC
                                                                                                                                                                                              GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGA
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                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application PC/TUS9906742
GENERAL INFORMATION:
APPLICANT: Ruffner, Duane E.
APPLICANT: Enferce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: T6678.PCT
CURRENT APPLICATION NUMBER: PCT/US99/06742
CURRENT FILING DATE: 1999-03-28
EARLIER APPLICATION NUMBER: 60/079,792
EARLIER FILING DATE: 1998-03-28
SAFTWARE: WORD97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 603; DB 1;
Pred. No. 1e-166;
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100.0%; Pred. No. 16.
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PCT-US99-06742-7
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Best Local Similarity
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PCT-US99-06742-7
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MOLECULE TYPE: I
ORIGINAL SOURCE:
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tct 961
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                                                                                           1230 ACCGCTGGTAGCGGTGGTTTTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA 1289
TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
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PPLICANT: Ahlijnian, Michael K
TITLE OF INVENTION: Transgenic Animals Expressing Human p25
FILE REFERENCE: PC10142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 603; DB 44; Lengtn 2.
Pred, No. 1.1e-166;
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                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/118,478
CURRENT FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0 - beta
                                                                                                                                                                                                                                             Sequence 5, Application US/60118478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Escherichia coli
US-60-118-478-5
                                                                                                                                                1290 TCT 1292
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1230 ACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA 1289
                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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restriction enzyme HindIII"
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sequence of E. coli
expression plasmid
pOC 56/RBS II, NcoI"
                                                                                                                                                                                                                                                                                                                      APPLICANT: Haas, Werner
APPLICANT: Hunziker, Willi
TITLE OF INVENTION: SOLUBLE KIT LICANDS
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RAN 4105/142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
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APPLICATION NUMBER: EP 91810609.7
FILING DATE: 30-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KASE, Alan P.
REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                         US-07-919-535C-26; Sequence 26, Application US/07919535C; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: DOS 4.0
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COCATION: 1.2577
OTHER INFORMATION: Sequen
CTHER INFORMATION: Sequen
CTHER INFORMATION: POC 5:
US-07-919-535C-26
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
CONWINY: United States
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
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LOCATION: 121..126
OTHER INFORMATION: /not
OTHER INFORMATION: rest
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LOCATION: 141..146
OTHER INFORMATION: /not
OTHER INFORMATION: rest
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FILING DATE: 19920723
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                                                     930 GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGGTTCAGCCCGACCGC 989
                      Gaps
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  Length 2577;
                      Indels
39.0%; Score 603; DB 3; Le
100.0%; Pred. No. 1.1e-166;
Live 0; Mismatches 0;
           al Similarity 100.
603; Conservative
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DKF2p434C AU081137 601125429

DKFZp434H

Homo sapi AV735756 DKFZp434E V120B11 m 601123218

V131C11 m 4A3A-P8F1

4A3A-P8A1 601123369

4A3A-P2G2

AL593919

M902H11 m DKFZp434A N900E9 mT

AU081124

602636869

601123114 V153C6 mT 4A3A-P9E3 ASIR0004

601123112 DKF2p4340

DKFZp434G

30-JUN-2000

Homo sapi

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Run

Sequence:

Title:

Searched:

Database

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Eukāryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Anopheles.
1 (bases 1 to 1004)
1 (bases 2, Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae pilot gene discovery project: identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /.strain="MA r/r"
/strain="MA r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
/clone=lib="Anopheles gambiae immune competent 4A3A"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                 4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
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AG101654
AG101654
AV735756
AC04413
AC0875006
BE749123
AG685100
AC0431919
AL043840
AQ491919
AU081124
BE749090
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AJ281699
BF381364
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AL042334
AG000621
AL043585
AQ876001
BE737278
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BF664532
AL593919
AJ281376
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BE749172
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Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
Location/Qualifiers
1. .1004
/organism="Anopheles gambiae"
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                                                                                                                                                                                                   AQ491918
AU081124
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BF664532
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BE749123
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AJ281699
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AL042334
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BE737278
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AU081137
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 AJ281449 4A3A-P4D5
AJ281552 4A3A-P6F1
BE749097 601123138
BE749118 601123194
BE749178 601123194
AQ876011 V132B5 mT
AJ281661 4A3A-P8G1
ALO44178 DKEZP4344
AJ28150 4A3A-PBG1
AJ2816120 4A3A-PBG1
                                                                           (without alignments)
2556.972 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution.
                                                                                                                        1 GGTACCTGCCACCATGGCGC......CTCGCACAGCCTCTCCCACA 1547
                                                                  Search time 6501.33 Seconds
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          GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                       11351937 seqs, 5372889281 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 January 17, 2002, 08:54:22
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Gapop 10.0 , Gapext 1.0
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and is derived by analysis of
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          polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from the Groward priming site which reads from the 3' end of the CDNA. The 4A3A is a directionally cloned and normalized CDNA library that was constructed from the 4A3A cell line oigo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                           GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC 869
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AJ281449
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                                                                                                                                                                                                                                                                                                   38.6%; Score 597.2; DB 10; Length 1004; 99.3%; Pred. No. 1e-160; Live 0; Mismatches 4; Indels 0;
                                                                                                             2 others
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AJ281449.1 GI:6929329
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/clone_ib="Anopheles gambiae immune competent 4A3A"
/cell_line="immune competent 4A3A"
/tlab_host="s. coli DH10B"
/note="Vector: pT7130-pac (Pharmacia) with a modified
/note="Vector: pT7130-pac (Pharmacia) with a modified
/note="Vector: pT7130-pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
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                            Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
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                          Scheetz, T., Roberts, C
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European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
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Pred. No. 1.4e-160;
0; Mismatches 4;
                       Casavant, T.L., Chang, S.,
                                                                                                                                                                                                                                                                                                                                                                                gambiae"
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/clone="4A3A-P4D5"
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/organism="Anopheles
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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1 (bases 1 to 1070)
Dimpoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) 20300950
                                  4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
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European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
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ilarity 99.5%; Pred. No. 2.9e-159;
Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                    African malaria mosquito.
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AJ281552.1 GI:6929432
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; 1 (bases 1 to 756)

I (bases 1 to 756)

I (bases 1 to 756)

I (butpicher)/mgc.nci.nih.gov/.

I unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM140 row: k column: 09
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                                                                                                                                                                                                                                             996 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA 1055
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                             GTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC
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/db_xref="taxon:9606"
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High quality sequence stop: 739.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE749147 959 bp mRNA EST 15-SEP-2000 601123315F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:3348291 5'
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                                                                                                            ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGGACAGGACTATAAA
                                                                                                                                                          GATACCAGGCGTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGC
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                                               Length 756;
                                                                       Indels
                                               DB 10;
                                                                         16;
                                               Score 585.4; DB 10
Pred. No. 2.4e-157;
                                                                       0; Mismatches
 174
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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 207
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                                               37.8%;
97.3%;
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BE749147
BE749147.1 GI:
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AUTHORS
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JOURNAL
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/clone="INAGES:348291"
/clone="INAGES:348291"
/clone="Ib="NIH_MGC_5"
/tissue_type="carcinoma cell line"
/lab_host="arcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAGGG; Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
45 a 229 c 252 g 233 t
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM140 row: n column: 04
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97.1%; Pred. No. 7.4e-157.
tive 0; Mismatches 17.
                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                         High quality sequence start: 13
High quality sequence stop: 800.
Location/Qualifiers
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cDNA Library Preparation: Ling Hong/Rubin Laboratory

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134 ATCT 131
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AUTHORS
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COMMENT
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/lab_host="DH10B (phage-resistant)"
/note="Corgan: carcinoma cell proff; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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<del>...</del>
                                                                                                                                                                                                             Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI40 row: k column: 23
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
1.759
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 759)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                              BE749118 759 bp mRNA EST 15-SEP-2000 601123194F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:3348238 5'
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98.7%; Pred. No. 6.6e-156;
Live 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3348238"
/clone_lib="NIH_MGC_5"
                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
131 TTACGCGCAGAAAAAAAGGATCT 109
                                                                                                                                              BE749118.1 GI:10163110
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BE749118
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Euteleostomi;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G. E. Consortium/ILNL at: image.llnl.gov Plate: LLCM140 row: h column: 11
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CTGCGCCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC 1048
                                                                                                                                                               GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGC 1168
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE749178 840 bp mRNA EST 15-SEP-2000
601123444F1 NIH_MGC_5 Homo sapiens CDNA clone IMAGE:3348154 5'
                     <u> ACTGGCAGCAGCGCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA</u>
                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

(bases 1 to 784)

Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ876119 784 bp DNA GSS 08-NOV-1999 V133E1 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', DNA sequence.
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                                                                                                     GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC
                                                                                                                                                        GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAA
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Length 840;
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                           Indels
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; DB 10;
1.7e-155;
ches 5;
                           0; Mismatches
Score 579;
Pred. No. 1
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te of mTn-3xHA/lacZ insertion.
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Yale University
P.O. Box 208103, New Ha
Tel: 203 432 9949
Fax: 203 432 6161
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37.4%;
99.1%;
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Unpublished (1999)
                           Conservative
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              Similarity
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AQ876119.1
  Query Match
              Best Local
Matches 58
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AQ876119/c
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COMMENT
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/clone_lib="mmn-3xHA/lacz Insertion Library, strain Y2278"
/lab_host="E." coli"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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Insertion Library, strain Y2278 Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGTATGTAGTAGCGGCGTGCTACAGAGTTGTT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 755 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC
                                                                                   /organism="Saccharomyces cerevisiae"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT
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                                                                                                                                                                                                                                                                                                                                                                               1 others
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V132B5 mTn-3xHA/lacZ Insertion Libra
cerevisiae genomic 5', DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                               186
Seq primer: GGCCTTCTTTCTTGGAAGTAC Class: transposon-tagged.
Location/Qualifiers
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/strain="4A r/r"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               African malaria mosquito.
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99.3%;
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1 (bases 1 to 617)
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Best Local Similarity 99.3
Matches 578; Conservative
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AJ281661
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/clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pHSS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mfn 3xHA/lacz minitransposon containing lacz, URA3, and tet resistance.
                                                                                                                                        Ross Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., destrages, S.A., Cheung, K.-H., Shechan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                            Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
1 (bases 1 to 795)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                795 ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGCCGAA 736
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Pred. No. 6e-154;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                          Gray Court of Market State of Market State of Market State S
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/organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: anuj.kumar@yale.edu
te of mTn-3xHA.lacz insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
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Best Local Similarity 99.1%;
Matches 576; Conservative
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/colone="4A3A-P8610"
/clone="14A3A-P8610"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/clone_lib="Immune competent 4A3A"
/clone_lib="Immune competent 4A3A"
/clone_lib="E. coli bH10B"
/lab_host="E. coli bH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: EcoRI; Site_2: Not!; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukāryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
and Kafatos,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000).
                                                                                                                                                                                                                                                                                                                              4A3A-P8G10-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P8G10, mRNA sequence.
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Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrass 1, 69117 Heidelberg, Germany.
Location/Qualifiers
                                                                                                 1252 TIGITIGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT 1292
                                                                                                                                                                      215
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Pred. No. 1.5e-151;
0; Mismatches 3;
                                                                                                                                         255 TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Wall. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990 IGCGCCITATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG 1109
                                                                                                                                                                                                                                                       690 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA 749
                                                                                                                                                                                        4A3A-P1H1-F Anopheles gambiae immune competent 4A3A Anopheles
                                                                                                                         930 GIGIAGGICGIICGCICCAAGCIGGGCIGIGIGCACGAACCCCCCGIICAGCCCGACCGC
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                                                                                                                                                                                                                                      810 GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC
                                        Length 571;
                                                                        Indels
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                                            DB 10;
                                                                          3;
                                          Score 555.2; DB 10
Pred. No. 1.1e-148;
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Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
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Anopheles gambiae
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99.5%;
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                                                                             557; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin.
6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (Mational Research Centre for Biotechnology Ltd Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                          990 TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
                                                                                                                                                                                                                                                                                                                                                           CIGCIGAAGCCAGITACCITCGGAAAAAGAGITGGTAGCTCTTGATCCGGCAAACAAAC 1229
                                                                                                                                                                                                                             CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG 1109
                                                                                                                                                                                                                                              11 TITCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCG 276
GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC 216
                                TITCICCCTICGGGAAGCGIGGCGCTITCICAAIGCICACGCTGIAGGIAICICAGIICG 929
                                                                                              GIGIAGGICGIICGCICCAAGCIGGGCIGIGIGCACGAACCCCCGIICAGCCCGACCGC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALU44178 571 bp mRNA EST 29-FEB-2000 DKFZp434P0828_s1 434 (synonym: htes3) Homo sapiens CDNA clone DKFZp434P0828_3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                            EST (Bloecker, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced g1:5866789.
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Genome Project.

No r1 sequence available.

This clone (DKF2p434p0828) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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168 c 149 q 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
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/db_xref="taxon:9606"
/clone="DKF2p434P0828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 571)
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/lab_host="DH10B"
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/clone_lib="min-sxHA/lacz Insertion Library, strain Y2278"
/lab_host="E. coli"
/note="vector: pHSS6-Sal; A yeast genomic DNA library
without Z micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a min-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
                                                                                     Saccharomyces cerevisiae
Eukaryota: Fungi; Ascomycota: Saccharomycotina: Saccharomycetes:
Saccharomycetales: Saccharomycetales: Saccharomycetales:
Saccharomycetales: Saccharomycetales: Saccharomyces.

( Dasss 1 to 794)

Ross-Macdonald, P., Roemer, T., Coelho, P.S. R., Agarwal, S., Kumar, A., Gestigaes, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
Unpublished (1999)
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/db_xref="taxon:4932"
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Tel: 203 432 9949
Fax: 203 432 6161
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98.3%; Pred. No. 2.6e-148;
11ve 0; Mismatches 8;
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
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Class: transposon-tagged
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Matches 579; Conservative
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                                                                                                                      /Strain="4A r/r"
/db_refe* terms parameter
/db_refe* terms refe* t
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69117 Heidelberg, Germany.
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98.1%; Pred. No. 2.4e-148;
11ve 3; Mismatches 8;
                                                                                               /organism="Anopheles gambiae"
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RESULT 13 AQ875988/c LOCUS DEFINITION

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Homo sapiens CB library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion" 176 c 159 g 147 t 4 others
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 615)
                                                               1184 TACCTTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGG 1243
 GCCTAACTACGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                 AV735664 615 bp mRNA EST 17-OCT-2000
AV735664 CB Homo sapiens cDNA clone CBNAME07 5', mRNA sequence
AV735664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748 GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC 807
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                                                                                  CTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghal Hematology Institute
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ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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                                                                                                                              1244 TGGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
                                                                                                                                              248 TGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBNAME07"
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                                                                                                                                                                                                                                                                                              AV735664.1 GI:10853245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 86-21-64740490
Fax: 86-21-64743206
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 954)
Ansorge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No rI sequence available.
This clone (DKFZp434C1Z) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Am Klopferspitz 18a D-82152 Martinsried, Germany
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Tanana Genome Analysis, German Cancer
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187 CCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT 246
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253 g 214 t
                                               988 GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC
                                                                                                                                                                                                                                                   1048 CACTGGCAGCACCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG
                                                                                                                                                                                                                                                                                                                                                                                 /clone="DKFZp434C172"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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DKFZp434C172_s1 434 (synonym: hi
DKFZp434C172 3', mRNA sequence.
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273 c 25
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Unpublished (1999)
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                                                                                                                                             TITCICCCTICGGGAAGCGIGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCG 929
                   Gaps
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                                                                                                                     GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC
                                                                       750 CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT
                                                                                                          GGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC
                  ó;
Length 954;
                  Indels
Score 550.2; DB 10;
Pred. No. 3.5e-147;
0; Mismatches 3; 1
Query Match 35.6%;
Best Local Similarity 99.5%;
Matches 552; Conservative
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Search completed: January 17, 2002, 08:54:31 Job time: 7143 sec

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January 17, 2002, 11:50:28; Search time 10436.3 Seconds (without alignments) 2856.404 Million cell updates/sec
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1 GGTACCTGCCACCATGGCGC.......CTCGCACAGCCTCTCCCACA 1807
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	LOR875 PiAN7 CLODIO VOOR99 CLODING vec X14353 Plasmid pi- LOR918 Pi-VX CLODIO 107209 Sequence 3 AR00212 Sequence 8 AR12228 Sequence 6 AR12228 Sequence 5 AR12228 Sequence 6 AR12228 Sequence 7 AR12228 Sequence 7 AR12228 Sequence 17 AR03312 Sequence 17 AR03307 Sequence 17 AR03684 CLODING v AF086841 CLODING v	AF086848 Cloning v AF086850 Cloning v AF086851 Cloning v AF086852 Cloning v AF087552 Cloning v AF087562 Cloning v AF087564 Cloning v AF087565 Cloning v AF087566 Cloning v AF087566 Cloning v AF087666 Cloning v AF087666 Cloning v AF087666 Cloning v AF087666 Cloning v	In 26-JUL-1993
		· w	circular SYN  con were supplied to  the GenBank Currato  #TYPE DNA CIRCULAR
ΔI	TYNITY THE PLAY X V V V V V V V V V V V V V V V V V V	AF086849 AF086850 AF086851 AF086852 AF087563 AF087564 AF087566 AF087566 AF087565 AF087565 AF0876664 AF087666	DNA
DB		00000000000000	885 bp vector. 110776 110776 110776 110776 110776 110776 110776 11077 1107
Length	885 902 902 2933 7253 7253 7253 7253 6028 6028 6028 6031 1173 1173 1173 1173 1173 1173 1173 1	1199669 1199669 1199669 1199669 1199669 1199699 1199699	885 bp ning vector. GI:310776 construct DN construct 1 sequence. 1 to 885) from VecBase ed (1991) from Vecbase ed (1991) and their a nder the ausp ector. N7 - Cloning
Query Match			IAN7V 7 Clo 775 75.1 75.1 hetic ficial bases bases bases bases bases bases ficial fici
Score	7 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		
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<b>1</b> 24			

1173

1113

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ATPIVX 902 bp DNA SYN 28-SEP-1992 Cloning vector pi-VX used for screening bacteriophage lambda gene libraries for specific DNA sequences in Escherichia coli. Probe sequences are inserted in the vector pi-VX. Contains a polylinker, and origin of replication (derived from pMB1) and a tyrosine amber-suppressor gene (synthetic supF gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suppressor gene.

Cloning vector pi-VX.

Cloning vector pi-VX.

Cloning vector pi-VX.

Cloning vector pi-VX.

artificial sequence; vectors.

1 (bases 1 to 902)

Samilatis,T., Fritsch,E.F. and Sambrook,J.

Molecular cloning

(in) Maniatis,T., Fritsch,E.F. and Sambrook,J. (Eds.);

Molecular cloning

(in) Maniatis,T., Fritsch,E.F. and Sambrook,J. (Eds.);

Molecular cloning

(in) Maniatis,T., Fritsch,E.F. and Polisky,B.

(in) Maniatis,T., Fritsch,E.F. and Sambrook,J. (Eds.);

Molecular cloning

(in) Maniatis,T., Fritsch,E.F. and Sambrook,J. (Eds.);

(in) Maniatis,T., Fritsch,E.F. (Eds.);

(in) Maniatis,T., Fritsch,E.F. (Eds.);

(in) Maniatis,T., Fritsch,E.F. (Eds.);

(in) Maniatis,T., Fritsch,E. (Eds.);

(in) Maniatis,T., Fritsch,E. (Eds.);

(in) Mania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 IGAAGIGGIGGCCIAACTACGGCTACACTAGAAGGACAGTATITGGTATCTGCGCTCTGC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 CGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAAGT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTAGCGGTGGTTTTTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT 1292
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                                                                                                  CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGG
                                                                                                                                                                                                                                                                             1054 CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning vector; origin of replication; plasmid; polylinker;
AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 41.8%; Score 756.2; DB 12; Length 902; al Similarity 98.1%; Pred. No. 9.5e-209; 790; Conservative 0; Mismatches 3; Indels 12;
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/db_xref="taxon:31856"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECORI-Smal-BamHI-Sall-Pstl-BglII-xbal-HindIII SELECTION
                                                                                                                                                                                                                                   COMMENT
                                                                                                                                 information from New England Biolabs COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGCAGATTAGAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACCACGGTAATGCTTTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGATITAGAGICTGCTCCCTITGGCCGCTCGGGAACCCCACCACGGGIAAIGCTITT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VecBase(3):pBR322, VecSource(3):Poly8, GenBank(50):EcoTgy
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                                                                                                                                                                                                                                                                                                              The polylinker of PiAN7 contains additional BglII and XbaI
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                                                                                                                                                        Obtained 12-SEP-1986 from New England Biolabs
by magnetic tape
by magnetic tape
16-DEC-1986 by F. Pfeiffer:
449,450. Ar' to 'TA' to match revised sequence of
PIAN7 is thought to replace PivX.
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Pred. No. 2.6e-211;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/db_xref="taxon:32630"
239 c 236 g 217 t
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1-202 202- 1 (192-225-225-2340-880 2522-3162
            16-DEC-1986
                                                                                                                                         #citation sequence
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Best Local Similarity 95.9%;
Matches 805; Conservative
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                                                              artificial
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                                    ACCESSION VB0066
SOURCE artific
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Query Match 41.8%;
Best Local Similarity 98.1%;
Matches 790; Conservative
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Nucleic Acids Res. 11 (8), 2427-2445 (1983)
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Plasmid synthetic construct
artificial sequence.
1 (bases 1 to 902)
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artificial sequence;
suppressor transfer R
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                                                                                                                                                                                                                                                               Length
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Pred. No. 9.5e-209;
0; Mismatches 3;
/organism="synthetic construct"
/plasmid="pi-VX"
/db_xxef="taxon:32630"
1..109
                                                                                                                                                             replication"
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/note="suppressor tRNA"
213. .902
/note="origin of replic
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                                                              1. .109
/note="polylinker"
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KEYWORDS

RESULT

SOURCE

COMMENT

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VecBase(3):pBR322, GenBank(50):EcoTgy, VecSource(3):OriMB1
                                                                                                                                                                                                                                                                                                                                                          #checksum 9265
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Pred. No. 9.5e-209;
0; Mismatches 3;
                                      VecBase(3):PiAN7, VecBase(3):mWB2344

    .902
/organism="synthetic construct"

                                                                                                                                                                                                 Conflict (cfl) and Mutations (mut): PiVX source
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TAC 492-94 OriMB1
TAC 3013-15 pBR322
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250 c 237 g
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SUMMARY PivX #length 902
Location/Qualifiers
                                                                           Features pf Pivx (902 bp)
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Best Local Similarity 98.1%;
Matches 790; Conservative (
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cfl 811-12 T.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetic and Physical Studies on the replication of ColE1-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The ATCC strain 39083 contains PiVX in combination with plasmid
                                                                                                                                                                                                                                                          Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Currator Program. Pi-VX
Cloning vector used for screening bacteriophage lambda ENTRY PIVX
#TYPE DNA CIRCULAR
TITLE Pi-VX - Cloning vector used for screening bacteriophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Backman K., Betlach M., Boyer H.W., Yanofsky S. Cold Spring Harb Symp Quant Biol 43, 69-76 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN OF REPLICATION KEYWORDS
                                               SYNPIVXV 902 bp DNA circular SYN 26-JUL-1993
Pi-VX cloning vector used for screening bacteriophage lambda.
L08918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maniatis T., Fritsch E.F., Sambrook J.
(IN) Maniatis T., Fritsch E.F., Sambrook J.;
MOLECULAR CLONING: 353-361;
BOLD SPRING HARBOR LABORATORY (1982).
BASES 1 TO 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Nucl. Acids Res. (1983) 11: 2427-2445 #title
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synthetic construct
artificial sequence.
1 (bases 1 to 902)
gilbert, W.
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polylinker \
origin of replication
CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE artificial COLLECTION ATCC 39083
                                                                                                                                                                                                                                                                                                                                                                                   DATE 17-DEC-1982
ACCESSION VB0010
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#title
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source 1- 34 ppR322 1- 115 pivX-Polylinker 207- 1 (c) Tyr-tRNA synthetic (GenBank(50):EcoTgy) 1- 583 0riMB1 2522-3104 pbR322
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387 TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
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artificial sequence.
1 (bases 1 to 3392)
Maruyama, K. and Sugano, S.
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                                                                                 1071 AGGATTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 1130
                                         1131 TACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 1190
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            469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGGGGGAAGGATTCGAACCTTCGAA
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Pred. No. 2.2e-208;
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Seed, B.D.D.o.M.B., Allen, J., Aruffo, A., C
Oquendo, C.P., Simmons, D., Stamenkovic, I.
Rapid immunoselection cloning method
Patent: EP 0330191-A2 3 30-AUG-1989;
Location/Qualifiers
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699 c 682 q
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97.6%;
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Sugano, The Institute of Medical Science, University of Tokyo, Department of Virology; 4-6-1, Shirokanedai, Minatoku, Tokyo 108, Japan (E-mail:ssugano@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                           ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
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267 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTA
                                                                                                                                                                                                             ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
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                                                                                                        ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA
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complete sequence
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Maruyama, K. and Sugano, S.
PME168-FLJ: a versatile expression vector
Published Only in DataBase (1997) In pres
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/db_xref="taxon:29278"
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Expression vector pME18S-FL3,
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                                               1008 AGCCGGCGCTTACTGGCACTTCAGGAACAAGCGGGGGCGCTGCTCGACGACGCCGAAG
                                                                                                        1068 CCATGCTGGCGGAGAATCATAGCACTTCGGTGCCGAGGACGACGACGACTGGCGCTCAT
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290 TGTAGTCAGAGCCCCCGGGCAGCACAGGCCAATGCCCGTCCTTCCCCTGCAGGATGAGTA
                                                                                                                                                                                350 GTGAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCCT---
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                                    AGCCGGCGCTTTACTGGCACTTCAGGAACAAGCGGCGCCCTTAAGGGCCCATATGGTGAGT
                                                                                   GGATGC-------CTTGACCCCAGGCGGGATGGGGGAGACC
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                                                                                      780 GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTTCCTGTTCCG
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2028 AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGCCTACACTAGAAGGACAGT
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                                                                                                                                                                                                                                                                                                                                                          drifficial sequence.

I (bases 1 to 725)

Carroll, M.W. and Mitrophanous, K.
Equine infectious anaemia virus (elav) based
Patent: WO 9932646-A 57 01-JUL-1999;
CARROLL MILES WILLIAM (CB); MITROPHANOUS KYRIACOS
LOCATION/Qualifiers
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/db_xref="taxon:32630"
/note="complete sequence of pSC65"
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Pred. No. 2.1e-165;
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WO9932646.
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97.5%;
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Best Local Similarity 97.5'
Matches 617; Conservative
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GI:14106605
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Best Local Similarity 91.4%;
Matches 638; Conservative
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5482 AGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
                              655 TAAAGIGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGGTTGCTGCCGTTTTTCCATA
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                    1140 ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAAA
                                                              595 TITTACTGGCCTGCTCCCTTATCGGGAAGCGGGCGCGCATCATATCAAATGACGCGCCGCTG
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Collins, M.K., Weiss, R.A., Takeuchi, Y. and
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Pred. No. 1.6e-164;
                                                                                                                                                                            A60212 5865 bp DNA circular
Sequence 8 from Patent W09708330.
A60212
A60212.1 GI:3715220
                                                                                                        AAGCAGCAGATTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                  0; Mismatches
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Patent: WO 9708330-A 8 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                               1373
                                                                                                                                                                                                                                                                                                                                           /organism-"unidentified"
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1602 c 1390 g 1
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91.4%;
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Matches 638; Conser
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Collins, M.KatherineLevinge, Weiss, R.Anthony, Takeuchi, Y. and
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Pred. No. 1.6e-164;
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Patent: US 6165715-A 8 26-DEC-2000;
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Sequence 8 from patent US 6165715.
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4275 GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCCTTATCCGGTAACTATCGTC 4334
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                                                   GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 1194
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Pred. No. 1.6e-164;
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Sequence 5 from Patent WO9708330.
A60209
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Collins,M.K., Welss,R.A., Takeuchi,Y.
EXPRESSION SYSTEMS
CALCE: WO 9708330-A 5 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
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                   4335 TIGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCAGCAGCTGGTAACAGGA
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Collins, M. KatherineLevinge, Weiss, R. Anthony, Takeuchi, Y.
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Collins,M.K., Welss,R.A., Takeuchi,Y.
EXPRESSION SYSTEMS
Patent: WO 9708330-A 6 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
Location/Qualifiers
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4308 GCTGTGTGCACGAACCCCCCGTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC
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Collins, M. Katherine Levinge, Weiss, R. Anthony, Takeuchi, Y.
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Pred. No. 1.6e-164;
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ilarity 91.4%;
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Patent: US 6165715-A
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1 (bases 1 to 6312)
Collins, M.K., Weiss, R.A., Takeuchi, Y. and Cosset, F. EXPRESSION SYSTEMS
Patent: NO 9708330-A 7 06-MAR-1997;
CANCER RES CAMPAIGN FECH (GB)
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ilarity 91.4%; Pred. No. 1.6e-164;
Conservative 0; Mismatches 60;
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Collins, M. Katherine Levinge, Weiss, R. Anthony, Takeuchi, Y. and
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TTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGC
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Patent: US 6165715-A 7 26-DEC
Location/Qualifiers
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Nucleotide sequenc Nucleotide sequenc PEE12 Combo BM 12 Complete nucleotid ColE1 origin of re Vector pAS11b DNA. Plasmid pSP72. ES

Plasmid FBdelPGASA TF8-5G9 CDR-grafte TF8-5G9 CDR-grafte

FBdelPASAF FBdelPMOSA

Plasmid

Expression plasmid Vector puC28 nucle Plasmid pTRP. Syn plasmid pTRP. Syn plasmid BGINV. Sy pBGINV plasmid use plasmid P\_L-mu-smc

Nucleotide sequenc Transgenic unc-119 pGHRH-4 44Sk const Plasmid pDS5/RBSII

Universal reporter DNA encoding gluta Plasmid GHRH1-29YA pBC66-01, containi

DNA target sequenc

Expression plasmid pDS56/RBSII-1 sequ Expression plasmid Plasmid pDS56/RBSI

pDS56/RBSII-2 sequ

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Vector; vaccine; tumour; antigen; plasmid pITL-1; ds.
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Chimeric - Escherichia coli.
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HUMAN SERVICES

Plasmid pITL-1 comprises a base vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH 10-beta/PP is deposited as ATCC 98400. Novel vectors comprise a lubera/PP is deposited as ATCC 98400. Novel vectors comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site (see AAV21735-36) which accepts CDNA products from RT-PCR cloning. They also contain minmal non-human components, such as a replication origin (see AAV21715) and selectable matter gene (see AAV21717-18) that are necessary for production of the vector. The novel vectors are used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immune response in immune response to the traget sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as subjusted to the vectors. The target antigens are expressed as self polypeptides or peptides and appropriately presented on antigen presented. unised polynucleotide vectors – comprising human derived promoter sequence acceptance site, used for the production of vaccines presented on antigen presenting cells. Claim 14; Page 56; 125pp; English. DEPT HEALTH & Nelson PJ; WPI; 1998-159552/14  $\Omega$ S Nelson EL, Humanised (USSH) and 

Sequence 1807 BP; 419 A; 463 C; 492 G; 433 T; 0 other;

·; TCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCGCTTGTCCTAATAAAATTAAGTT 420 Gaps TATCAGTGATAAAGTGTCAAGCATGACAAAGTTGCAGCCGAATACAGTGATCCGTGCCGG 120 GCCATATGGTGAGTGGATGCCTTGACCCCAGGCGGGGATGGGGGGAGACCTGTAGTCAGAG 300 gccatatggtgagtggatgccttgaccccaggcgggggatgggggagacctgtagtcagag 300 GCATCATTTTGTCTGACTAGGTGTCCTCTATAATATTATAAGCTTGATATCGAATTCTTT 480 9 GGTACCTGCCACCATGGCGCGGATTCTTTATCACTGATAAGTTGGTGGACATATTATGTT CCCTGGACTGTTGAACGAGGTCGGCGTAGACGGTCTGACGACGCAAACTGGCGGAACG GTTGGGGGTGCAGCAGCCGGCGCTTTACTGGCACTTCAGGAACAAGCGGGCGCCTTAAGG Length 1807; ; Indels 19; ö DB 100.0%; Score 1807; 100.0%; Pred. No. 0; ative 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 1807; Conservative 61 121 61 181 181 241 241 361 301 301 361 421 481 481 121 δy Dβ δ В óλ g οy g δ qq qq qq οy Qγ qq δλ δ

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1020 ctcagtgactcagtgagtaataaagactcagtgacttctgatcctgtcctaactgccact 1440 AAAACTAAGGATGTCAGCAGAAATTTTTCCACCATTGGTGCTTGGTCAAAGAGGGAAAC 1560 960 960 TGATGAGCTCACTCTAGATGAGAGCAGTGAGGGAGAGACAGAGACTCGAATTTCCGGA 1620 9 780 780 840 840 900 GGCCTGCTCCCTTATCGGGAAGCGGGGGCGCATCATATCAAATGACGCGCCGCTGTAAAGT GTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTTTCCATAGGCTCC gttacgttgagaaagaattcctgcagcccgccgcttgctggcgtttttccataggctcc GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGA CCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTC AATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT tgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagt CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA CTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG AGCAGCAGATTACGCGCAGAAAAAAGGATCTGGGGGATCCGGAGAGCTCCCAACGCGTT GGATGCATGGATGAGGGAAAGGAGGTAAGATCTGTAATGAATAAGCAGGAACTTTGAAGA CTCAGTGACTCAGTGAGTAATAAAGACTCCAGTGACTTCTGATCCTGTCCTAACTGCCACT CCTTGTTGTCCCAAGAAAGCGGCTTCCTGCTCTCTGAGGAGGACCCCTTCCCTGGAAGGT 601 721 541 661 961 1081 1141 1201 661 781 841 841 901 1021 1021 1201 1261 721 781 901 196 1261 1321 1321 1381 1441 1441 1501 1501 1561 1381 q δ P Qγ pp οy g Ω οg δŽ Ω Qγ g δy qq οy 셤 QΥ QQ Qγ Db QΥ Q ÓΫ qq q δλ a g ΩY ŏλ δy a Q

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                                                                                                                                  PITL-1 GFP comprises base vector pITL-1 (see AAV21733) and
                 a humanised green fluorescent protein (GFP) reporter sequence (see AAV21725). Novel humanised vectors comprise a human-derived promoter or mammalian homologue which is functional in mammalian target tissue and cells and a sequence acceptance site which
 GCTATITCAGITTICCGTTITGTGCAATITCACTTATGATACCGGCCAATGCTTG
                                                                  GTTGCTATTTTGGAAACTCCCCTTAGGGGATGCCCCTCAACTGGCCCTATAAAGGGCCAG
                                                                                   human derived
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                                                                                                                                                                                                                                                                                                                             AAV21734 standard; cDNA; 2308
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- Escherichia coli.
- Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 green fluorescent protein;
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973..1181
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
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AAV21734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAG 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                 used to express target antigens, especially tumour antigens. They are non-replicating in mammalian cells but are capable of extended stable expression of target sequences generating an immune response in immunised individuals. The vectors selectively elicit immune responses to the target sequences with little or no immune response to the other components of the vectors. The target antigens are expressed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and as such, presented on antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 GAACAAGCGGGCGCCTTAAGGGCCCATATGGTGAGTGGATGCCTTGACCCCAGGCGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 gtacaagtgagcgccttaagggccatatggtgagtggatgccttgaccccaggcggggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATGAGTAGTGGCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCACCACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1201 tggcgtttttccataggctccgccccctgacgagcatcacaaaaatcgacgctcaagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 gggggagacctgtagtcagagccccggggcagcacaggccaatgcccgtccttcccctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    700 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGACATCACAAAAATCGACGCTCAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        820 TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 ACCACGGGTAATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGACGCGCCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGC
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The novel vectors are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTTCGAAGTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCC
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                                                                                                                                                                                                                                                                                                           Sequence 2308 BP; 571 A; 601 C; 604 G; 532 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                              87.6%; Score 1583.2; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
accepts cDNA products from RT-PCR cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 1585;
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                                                                                                                2040
                                                                                                                                                                                                      1600 ACAGAGACTCGAATTTCCGGAGCTATTTCAGTTTTCTTTTCCGTTTTGTGCAATTTCACT 1659
                                                                                                                                            1300 CCGGAGAGCTCCCAACGCGTTGGATGCATGGATGAGGAAAGGAGGTAAGATCTGTAATG 1359
           1660 TATGATACCGGCCAATGCTTGGTATTTTGGAAACTCCCCTTAGGGGATGCCCTCA
                                                                                                                                       GATCCTGTCCTAACTGCCACTCCTTGTTGTCCCAAGAAAGCGGCTTCCTGCTCTGAGG
                                                                                                                                                            AGGACCCCTTCCCTGGAAGGTAAAACTAAGGATGTCAGCAGAGAAATTTTTCCACCATTG
                                                                                                                                                                 GTGCTTGGTCAAAGAGGAAACTGATGAGCTCACTCTAGATGAGAGAGCAGTGAGGGAAGAG
                                                                                                                                                                                       1120 GGTGGCCTAACTACGCCTACACTAGAAGGACAGTATTTGGTATCTGCGCGCTCTGGTGAAGC
       CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGT
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                                                                                                                                                                                                                                                                                                                                                        Vector; vaccine; tumour; antigen; plasmid pITL-A;
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472..680
/*tag= c
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Chimeric - Escherichia coli
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                                                                                                                                                                                                                                                                                                                                               Humanised vector pITL-A.
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plasmid pITL-A comprises a base vector for novel humanised polynucleotide vectors. The vector in Escherichia coli DH polynucleotide vectors. The vector in Escherichia coli DH polynucleotide vectors. The vector in Escherichia coli DH 10-beta/P3 is deposited as ATCC 98401. Novel vectors comprise a humanalian target tissue and cells and a sequence acceptance site in mammalian target tissue and cells and a sequence acceptance site They also contain minimal non-human components, such as a replication or face AAV21715. They also contain minimal non-human components, such as a replication or file vector. The novel vectors are are necessary for production of the vector. The novel vectors are are non-replicating in mammalian cells but are capable of extended are non-replicating in mammalian cells but are capable of extended standividuals. The vectors selectively elicit immune response to the target sequences with little or no immune response to the carget sequences with little or no immune response to the target sequences with little or no immune response to the components of the vectors. The target antigens are to the other components of the vectors selectively elicit immune response are processed as intracellular polypeptides or peptides and, as such, are processed as self polypeptides or peptides and appropriately are presented on antigen presenting cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised polynucleotide vectors - comprising human derived promoter and sequence acceptance site, used for the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TATCAGTGATAAAGTGTCAAGCATGACAAAGTTGCAGCCGAATACAGTGATCCGTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGTACCTGCCACCATGCGCGCGGATTCTTTATCACTGATAAGTTGGTGGACATATTATGTT
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                                               **tag= d
note= "ColE1 origin of replication"
1311..1547
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                                                                                                                                               promoter"
                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 56-57; 125pp; English.
"SupF gene"
                                                                                                                               /*tag= e
/note= "RANTES
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686..1292
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Best Local Similarity
Matches 1311; Conserva
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                                                                                 CGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAAGTCGATGACGGC
                                                                                                             AGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGTAATGCTTTTACT
                                                                                                                                       GGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGCCGCTGTAAAGT
                                                                                                                                                                                              GCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAG
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AAQ21163 standard; cDNA; 2932

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RESULT

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/note= "remnant of ASV LTR fragment (PvuII to MIul)" 948..1500
                                                                                                                                                                                                                                                                         enhancer'
                                                                                                                                                             /note=_______/note=_ "derived from synthetic tyrosine suppressor /note= "derived from synthetic tyrosine suppressor tRNA gene"
                                                                                                                                                                                                                                                                                                  tat responsive
                                                                                                                                                                                                                                                                                                                                                                        /note= "derived from SV40 origin of replication"
2918..2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CD53 cell surface antigen and DNA encoding it - for
immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
                                                cloning technique; CD2; cell surface antigen; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                      site
                                                                                                                                                                                                                                                        /function= enhancer
/note= "derived from cytomegalovirus AD169
1501..1650
                                                                                                                                                                                                                                                                                                                                                                                                    /note- "derived from pivx, remnant of R1 from polylinker"
1717..2569
                                                                                                                                                                                                                                                                                                                                           polylinker'
                                                                                                                                                                                                                                                                                                                                                                                                                                       "derived from pSV to splice and poly-A addition signals"
                                                                                                                                                                                                                                                                                     derived from HIV TATA and elements" 1651..1716
                                                                                                                            pMB1 origin"
                                                                                                                                                                                                                                                                                                                                           "derived from piLNXAN
                                                                                                                                                                                                                                                                                                                                   polylinker
                                                                                                                           from
                                                                                                                                                   /function= linker
/note= "SacII linker"
                                                                                         Location/Qualifiers
1..589
/*tag= a
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/note= "derived
590..597
                                 COS cell expression vector piH3
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2570..2917
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/note=
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                                                                                                  misc_feature
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                                                          tumour; ss
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                                                                                                                                                                                                                                                  Gaps
This COS cell expression vector was constructed from pisV (Little et al., Mol. Biol. Med. 1:473-488 (1983)) by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. The transcription unit consisted of a chimeric promoter composed of human cytomegalovirus AD169 immediate early peromoter composed of human cytomegalovirus AD169 immediate early enhancer sequences fused to the HIV LTR -67 to (plus)80 sequences. A polylinker confg. BetxI sites separated by a 350bp stuffer was inserted immediately downstream from the polylinker were placed the SV40 small bownstream from the polylinker were placed the SV40 small early region polyadenylation signals derived from pSV2. The new vector, which forms part of the wider disclosure of the specification, was used in the cloning of the human CD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCATAGGCTCCGCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                               GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCCTGGAAGCTCCCTCGTGCGCT
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                                                                                                                                                                                        Score 755; DB 13; Length 2932;
Pred. No. 3.3e-210;
0; Mismatches 15; Indels 4
                                                                                                                                                           Sequence 2932 BP; 775 A; 698 C; 682 G; 777 T; 0 other;
                                                                                                                                                                                                41.8%;
ilarity 97.6%;
Conservative (
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Best Local Similarity
Matches 788; Conserv
                                                                                                                                                 antigen gene.
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/*tag= j
/function= piVX, remnant of R1 site from polylinker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding CD19 cell surface antigen - useful for recombinant antigen prodn. for diagnostic and therapeutic purposes
                                                                                                                        CD19; cell surface antigen; T lymphocyte; immunoselection cloning;
                                                                                                                                                                                                                                                                                                                                                                             /function= psV splice and poly-Addition signals 2570..2917
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                                                                                                                                                                                                                                                                                                     /function= human cytomegalovirus AD169 enhancer
                                                                                                                                                                                                                                                                                                                                                   piLNXAN polylinker (HindIII to Xba)
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/note= "bases derived from pMB1 origin (pBR322
                                                                                                                                                                                                                                                                                                                                                                                                        of replication (Pvull
                                                                                                                                                                                                                                                                            /function= ASV LTR fragment (PvuII to MluI) 948..1500
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                                                                                                                                                                                                                                                                                                                                                                                                          SV40 origin
HindIII
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/function= SacI linker
(MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                     ocation/Qualifiers
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                                                           AAT38557 standard; DNA; 2932 BP.
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                                                                                                             Expression vector piH3.
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                                                                                                                                      vector; piH3; cyclic
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                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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misc_feature
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                    used in a novel immunoselection cloning method for cell surface antigen genes, e.g. human CD19 (see also AAT83856). This involves introducing CDNA fragments into the vector, transfecting mammalian cells in culture, maintaining the cells under conditions that allow antigen expression, exposing the cells to an antibody directed against the antigen, and recovering positive cells by contact with an immobilised antibody directed against the first antibody.
            Expression vector piH3 (AAT38557), deposited as ATCC 67634, can be
                                                                                                                                                                                                                                                                                                                                                                                                        469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA
                                                                                                                                                                                                                                GTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACGGGT
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                                                                                                                                           Length 2932;
                                                                                                                                                              15; Indels
                                                                                                         Sequence 2932 BP; 773 A; 700 C; 682 G; 777 T; 0 other;
                                                                                                                                         Score 755; DB 17;
Pred. No. 3.3e-210;
0; Mismatches 15;
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97.6%;
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Matches 788; Conservative
                                                                                                                                          Query Match
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/note= "bases 800-947 are derived from a remnant
of the ASV LTR fragment (PvuII-MluI)"
948..1500
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                                                                                                                                                                                 cloning; immunoselection; immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    origin of replication (PvuII-HindIII)
                                                                                                                                                                                                                                                                                                                                                                                        "bases 1-589 are derived from the pMB1 origin (pBR322 ori)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/note= "bases 1651-1716 are derived from the
piLNXAN polylinker (HindIII-Xba)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "bases 1717-2569 are derived from pSV to splice and poly-Addition signals" 2570..2917
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/note= "bases 948-1500 are derived from the
AD169 enhancer"
                                                                                                                                                                                                         therapy; diagnosis; vector; piH3; CD2; T-cell receptor; COS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic tyrosine suppressor tRNA gene (supF gene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "bases 590-597 are derived from
SacII linker"
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"bases 598-799 are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "bases 1501-1650 are derived
    and tat-responsive elements"
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
BP
AAT14702 standard; DNA; 2932
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89US-0379076.
90US-0553759.
93US-0139273.
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                                                                                        (first entry)
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/*tag=
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                                                                                                                                                                                 Cell surface antigen;
                                                                                                                                      Vector plasmid piH3
                                                                                                                                                                                                                            T-lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                        30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5506126-A
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                                                                                                                                                                                                                                                                            Synthetic
                                           AAT14702;
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                                             A NO NEW YORK NEW YOR
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Seed B;

Aruffo A,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA 948
                                                                                                                                                                                                                                                                                                                                               708
                                                                                                                                                                                                                                                                                                    469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                                                                                                                                                                                                                                Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins
                                                                                                  Vector piH3 (AAT14702) is a COS cell expression vector constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. This novel vector allows the generation of very large mammalian expression libraries and yields large amounts of protein in mammalian host cells, resulting in efficient selection. Efficiency of library construction is comparable to that achieved with phage lambda, but the clones generated are easier to manipulate. A novel immunoselection cloning method was used to clone genes (see also AAT14703-04 and AAT14706-26) for cell surface antigens of human lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTT
                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                            Length 2932;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                           Sequence 2932 BP; 774 A; 698 C; 683 G; 777 T; 0 other;
                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 97.6%; Pred. No. 3.3e-210;
Matches 788; Conservative 0; Mismatches 15;
                                                                                  Example 1; Fig 1A-B; 79pp; English.
                             WPI; 1996-200279/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1009
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/*tag= c
/note= "from synthetic tyrosine suppressor tRNA
. gene (supF gene)"
                                                                                                                                                                                  Vector; piH3; cell surface antigen; lymphocyte; human; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          / c== "SV40 small t antigen splice and early
region polyA signals from pSV2"
2570..2917
                                                                                                                                                                                                                                                                                                                                                                                            1501..1650
/*tag= f
/note= "HIV TATA and tat-responsive elements"
                                                                                                                                                                                                                                                                                                                                                                                  /note= "human cytomegalovirus AD169 enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "from piVX, remnant of R1 site from polylinker"
                                                                                                                                                                                                                                                 Location/Qualifiers
1..589
/*tag= a //ocfe= "from pMB1 origin (pBR322 ori)"
590..597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= i
/note= "SV40 origin of replication"
2918..2922
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= g
/note= "piLNXAN polylinker"
1717..2569
/*tag= h
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/note= "ASV LTR fragment"
/*E..1500
                                                                                                                                                                                                            Chimeric - Escherichia coli.
Chimeric - Human cytomegalovirus.
Chimeric - Human immunodeficiency virus.
Chimeric - Rhesus macaque polyoma virus.
                                                           1249 TTTTGTTTGCAAGCAGCAGATTACGC 1275
                                                                                                                                                                                                                                                                                              /*tag= b
/note= "Sali linker"
598..799
                                                                     92US-0983647.
88US-0160416.
                                                                                                                    AAV63441 standard; DNA; 2932
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                                                                                                                                                      07-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                       Expression vector piH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992;
25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_signal
                                                                                                                                       AAV63441;
                                                                                                                                                                                                                                                                                                                                                                        enhancer
                                                                                                                                                                                                 COS; ss
                                                                                                       RESULT 7
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889 TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGGTTCGGTGTAGGTCGTTCGCTTCAA
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                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of expression vector piH3, a COS cell expression vector constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SyMThetic transcription unit between the suppressor tRNA gene and the SyMT origin. The vector can be used in a novel method for cloning cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and immunoselection of cells expressing the antigen by adhesion to an antibody-coated substrate. The method is useful for the solation and molecular cloning of any protein which can be expressed and transported to the cell sufface membrane of a cukaryotic cell. It has been used to clone genes encoding cell surface antigens associated with mammalian T lymphocyte antigens cuch as CDL-53, LFA-3, LCAM-1, FCRI, TLisA and Leu8 (see AAV63442-63 and AAW80440-55). The invention provides high efficiency expression vectors, such as piH3, which allow the generation of very large mammalian expression libraries, and yield large amounts of protein in mammalian host cells, resulting in efficient selection. The cumunotherapeutic applications, including the diagnosis and immuner of immune mediated infections, diseases, and disorders of animals in colliding the diagnosis and animals and animals.
                                                                                                                                                                                                   New cloning vector and polylinker – based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;
                                                                                                                                                                                                                                                human lymphocyte antigenic sequences
                                                                                                                                                                                                                                                                                    Example 1; Fig 1A-B; 75pp; English.
890S-0379076
                   90US-0553759
97US-0861205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animals, including humans.
                                                                              (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                             WPI; 1998-609251/51
                                                                                                                      Seed B;
13-JUL-1989;
                                      21-MAY-1997;
                                                                                                                    Aruffo A,
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misc_feature
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                                                              588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 804 AGCAGATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA 745
                                  Gaps
                                                                                                                                             CICCIGITCCGACCCIGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
                                                                                                                              GTCGATGACGGCAGATTTAGAGTCTGCTCCTTTTGGCCGCTCGGGAACCCCACCACGGGT
                                                                                                                                                                                           AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCG
                                                                                                                                                                                                                                                       CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTT
                                                                                                                                                                                                                                                                                                                      TCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                  GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT
                                4;
    Length 2932;
                                Indels
 Score 755; DB 19;
Pred. No. 3.3e-210;
0; Mismatches 15;
Query Match
Best Local Similarity 97.6%;
Matches 788; Conservative
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469

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589 684

529

624 709

267 169 507

649

829

447

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1068
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                                                                                                                                             ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
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                                                                                                                                                                 83
                                                                                                                                                                                                     29
                                                                                                                                                                                   ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
                                                                                                                 AGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACT
                                     1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTA
                                                                                                                                                       /*tag= c
/note= "from synthetic tyrosine suppressor tRNA
gene (supF gene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "SV40 small t antigen splice and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "HIV TATA and tat-responsive elements"
                                                                                                                                                                                                                                                                                                                                                                   CD40; cell surface antigen; human; vector; plasmid piH3; cDNA library; COS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.589
/*tag= a
/note= from pMB1 origin (pBR322 ori)"
590.597
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/note= "human cytomegalovirus AD169
1501..1650
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/note= "piLNXAN polylinker'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/note= "ASV LTR fragment"
                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Escherichia coli.
Chimeric - Human cytomegalovirus.
Chimeric - Human immunodeficiency virus.
Chimeric - Rhesus macaque polyoma virus.
                                                                                                                                                                                                                          TTTTTGCAAGCAGCAGATTACGC 1275
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/note= "SalI linker"
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                                                                                                                                                                                                                                            TTTTTGTTTGCAGCAGCAGATTACGC 2
                                                                                                                                                                                                                                                                                             AAV81199 standard; DNA; 2932 BP
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                                                                                                                                                                                                                                                                                                                                     (first entry)
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/note=
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                                                                                                                                                                                                                                                                                                                                                        Expression vector piH3.
                                                                                                                                                                                                                                                                                                                                    10-MAY-1999
                                                                                                                                                                                                                                                                                                               AAV81199;
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                                                                                                                                                                                                                                                                                   AAV81199/c
                           949
                                             327
                                                                                                        1069
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                                                                                                                                             1129
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                                                                                                                                                                 147
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888

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1129 ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                                                                                                                                                                                                                                            1009 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTA 1068
                                                                                                                                                                                                                                                            949 AGCIGGGCIGIGIGCACGAACCCCCGIICAGCCCGACGCTGCGCCTIAICCGGIAACI 1008
                                                                                                                                                                                                                                                                                                                                             plasmid p1H3; vector; eukaryotic cell; COS; cell surface antigen; immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune disorder; infection; asthma; immune-complex disease; amyloidosis; multiple sclerosis; parasitic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA
GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT
                                                                                                                               CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "derived from SacI linker"
598..799
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function= "replication origin"
/note= "pBR322 ori from pMB1"
590.597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotic cell expression vector plasmid piH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Rhesus macaque polyoma virus. Chimeric - Escherichia coli. Chimeric - Human cytomegalovirus. Chimeric - Human immunodeficiency virus. Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTTGTTTGCAAGCAGCAGATTACGC 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1.589
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA50577 standard; DNA; 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoselection; panning; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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misc_feature
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                                            267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of expression vector piH3, a COS cell expression vector constructed from piSV by inserting a cell expression vector constructed from piSV by inserting a the SV4 origin. The vector can be used in a novel method for cloning cDNAs from mammalian expression libraries. The method is cloning cDNAs from mammalian expression libraries. The method is bysical selection of cells expression to antigen in enkaryotic cells and contains and molecular cloning of any protein contains and contains and molecular cloning of any protein contains and molecular cloning of any protein contains contains and molecular cloning of any protein contains contains and contains a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 ATCGAATTCTTTCGGACTTTTGAAAGTGATGGTGGTGGGGGAAGGATTCGAACCTTCGAA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    very large mammalian expression libraries, and yield large amounts of protein in mammalian host cells, resulting in efficient selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expression vectors for expression in eukaryotic cells or their fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGCTTTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGATGATTTACTGGCTGCTCCTTATCGGGAAGCGGGGCGCATCATATCAATGACGCGAAGCGGGCGCATCATATCAATGACGCGAAGCGGGCGCATCATATCAATGACCGCAAGCGGGCGCATCATATCAATGACGCGAAGCGGGCGCATCATATCAATGACGCC
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Stamenkovic I, Stengelin
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Best Local Similarity 97.6%; Pred. No. 3.3e-210;
Matches 788; Conservative 0; Mismatches 15; Indels
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          region polyA signals from pSV2"
2570..2917
                                                            /*tag= i
/note= "SV40 origin of replication"
2918..2922
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90US-0553759.
95US-0485447.
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89US-0379076.
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                                                                                         misc_feature
                                                                                                                                                                                                                         07-JUN-1995;
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13-JUL-1989;
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13-JUL-1990;
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The present sequence is that of COS cell expression vector plasmid piH3. The vector was constructed from piSV by inserting a synthetic transcription unit between the suppressor tRNA gene and the SV40 origin. The transcription unit consisted of a chimeric promoter composed of human cytomegalovirus AD169 immediate early connecter sequences fued to the HIV LRR +80 was inserted a polylinker. Immediately downstream from the LTR +80 was inserted a polylinker containing 2 BstXI sites separated by a 350 bp stuffer. The BstXI sites were flanked by XbaI sites, which could also be used to excise the insert. Downstream from the polylinker were placed the SV40 small tantigen splice and early region polyA signals derived compared in the vector can be used to construct large mammalian cDNA expression libraries. A new method for cloning cDNA encoding cell surface antigens is based upon transient expression of antigen in eukaryotic (e.g. COS) cells and physical selection of cells coated substrate such as a culture dish. The purified cDNA and the protein that it encodes are useful for imminodiagnostic and the protein transient expression of colls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding the CD19 cell surface antigen,
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                                                                                                                                                                                                                                                                to splice and poly-A site"
               "synthetic tyrosine suppressor tRNA gene"
                                                                                             /*tag= e
/note= "human cytomegalovirus AD169 enhancer"
                                                                                                                                            /*tag= f
/note= "HIV TATA and tat-responsive element"
                                                                                                                                                                                                                                                                                             /function= "replication origin"
/note= "from SV40 origin of replication"
2918..2922
                                                                                                                                                                                              /*tag= g
/note= "derived from piLNXAN polylinker"
                                               /*tag= d
/note= "remnant of ASV LTR fragment"
                                                                                                                                                                                                                                               /*tag= h
/note= "derived from pSV
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 'dene= "supF"
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89US-0379076.
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23-MAR-1990;
13-JUL-1990;
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                                                                                                                               TATA_signal
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                                                                                         Length 2932;
were designed for use in the novel methods of the invention
            yielding large amounts of protein in mammalian host cells, resulting in efficient selection.
                                                  Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;
                                                                                          Score 755; DB 21;
Pred. No. 3.3e-210;
                                                                                                       Pred. No. 3.36
0; Mismatches
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                                                                                          41.8%;
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Matches 788; Conserv
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New recombinant DNA encoding CD28 useful for diagnosing and treating immune-mediated diseases, infections or disorders, e.g. systemic lupus
                                                       Chimeric - Avian sarcoma virus.
Chimeric - Human oytomegalovirus.
Chimeric - Human immunodeficiency virus.
Chimeric - Rhesus macaque polyoma virus.
                                                                                                                                                                                            AD169 enhancer" 1501..1650
                                                                                           Location/Qualifiers
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/note=
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13-JUL-1990;
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/note= "Derived from the pSV2 splice and polyadenylation
                                                       Human, lymphocyte cell surface antigen; immune-mediated disease; asthma; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus erythematosus; platelet disorder; rheumatoid arthritis; transplant rejection; cyclic; circular; mutant; plH3; ds.
                                                                                                                                                                                                                                                                                                                                                                                              , uoue= "Derived from the HIV TATA and tat-responsive
elements"
1651..1716
                                 Expression vector piH3 DNA used to express human lymphocyte antigens.
                                                                                                                                                                                                                                                                                   /*tag= c
/note= "Derived from the synthetic tRNA gene (supF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Derived from pivx, remnant of R1 site from polylinker"
                                                                                                                                                                                                              /*tag= a
/note= "Derived from the pMB1 origin (pBR322 ori)"
                                                                                                                                                                                                                                            /*tag= b
/note= "Derived from the SacII linker (ACCGCGT)"
                                                                                                                                                                                                                                                                                                                                                                    /note= "Derived from the human cytomegalovirus
                                                                                                                                                                                                                                                                                                                          LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag* g
/note= "Derived from the piLNXAN polylinker
(HindIII to Xba)"
                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "Derived from a remnant of the ASV
fragment (PvuII to MluI)"
                    29-AUG-2001 (first entry)
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The present sequence for expression vector piH3 is used to provide high level expression of human lymphocyte cell surface antigens in eukaryotic host cells. Another expression vector piH34 (AASO3174) eukaryotic host cells. Another expression vector piH34 (AASO3174) c. sequences (AASO3172, AASO3173, AASO3175-AASO3195) are described relating to the invention of a novel method of clohing cDNA relating to the invention of a novel method of clohing cDNA relating to the invention of a novel method of clohing cDNA relating to the invention of a novel method of clohing cDNA relating to the invention of a novel method of clohing cDNA relating controlly and or comparison and efficient construction of cDNA mino acide extracellular domain sequence (amino acide 1-134 quven in amino acide vertacellular domain sequence (amino acide genes and the CD28 cDNA sequence (AASO3175) is also new. The purified genes and the CD28 cDNA sequence (AASO3175) is also new. The purified genes and applications, such as in the diagnosis and treatment of immune-mediated capplications or disorders in animals and humans. Such diseases diseases, infections or disorders in animals and humans. Such diseases include immune deficiency diseases, diseases of immediate type of include immune deficiency diseases, diseases of immediate type of include immune deficiency diseases, diseases of immediate type of include immune deficiency diseases, diseases of immediate type of complete tisorders, plasame and other cell neoplasms, parasitic diseases, planelled clasorders, plasame and other cell neoplasms, parasitic diseases, continue and purify other antibodies and antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACGCTGCGCCTTATCCGGTAACT 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICCIGITCCGACCCIGCCGCTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGGAGCAGCACTGGTA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGCGGGTTTT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGATGACGGCAGATTTAGAGTCTGCTCCCTTTGGCCGCTCGGGAACCCCACCACGGGT
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erythematosus, asthma, transplant rejection, rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2932 BP; 774 A; 699 C; 682 G; 777 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 755; DB 22;
pred. No. 3.3e-210;
0; Mismatches 15;
                                                             Example 1; Fig 1A-1B; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%;
97.6%;
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les 788; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 788;
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0 other;

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Sequence 7252 BP; 1942 A; 1686 C; 1751 G; 1873 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deletion in gag removes one or more adeleted gag gene. The deletion in gag removes one or more nuclectides downstream of nuclectide 350 of the gag coding sequence. One or more accessory genes are absent from the non-primate lenturius genome or lack the tat gene but includes the leader sequences between the end of the 5' long terminal repeat (LTR) and the ArG of gag. The vectors, particles or cells transfected with either of these, are useful for the delivery of nuclectides of interest to a target site (i.e. gene therapy). The retroviral vector can be used as a delivery system. Alternatively, a non-retroviral expression vector, adenovirus or plasmid can be used as a delivery system for the retroviral vector are troviral vector. The retroviral vectors are capable of transferring genetic material to non-dividing or slowly dividing cells. Deletion of larger regions of the gag gene in Equine infectious anemia virus (EIAV) vectors is advantageous and leads to higher titers of viral vector being produced. Deletion of accessory genes permits vectors to be produced without the genes normally associated with disease in lentiviral (e.g. HIV) infections. The deletion of these genes also permits the vector to
ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCGTA 1128
                                                  ACTACGCCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT 1188
                                                                                                   TCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT 1248
              Retroviral vector; non-primate; lentivirus; gag gene; tat gene; LTR; long terminal repeat; gene therapy; Equine infectious anemia virus; EIAV; HIV infection; MLV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention provides retroviral vectors derived from a non-primate
                                                              Retroviral vectors derived from a non-primate lentivirus genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitrophanous K;
                                                                                                                                                    TTTTTGTTTGCAAGCAGCAGATTACGC 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carroll MW, Kim N, Kingsman AJ,
                                                                                                                                                                  Examples; Fig 37; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                           AAX86928 standard; DNA; 7252 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0011037.
97GB-0027135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-GB03876,
                                                                                                                                                                                                                                                                                                                      Complete sequence of pSC65
                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                             20-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                            5301
                                                                                                                                                                                                                                                                                                                                                                               GTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG 1019
                                                                                                                                                                                                                                                                                                                                                                                              AGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1140 ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGA 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5182 ggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgttccg 5241
                                                                                                                                                                                       839
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                                                                                                                                                                                                                                                                                                                  CAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGT 959
                                                            TGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCTTGCTGGCGTTTTTCCATAGGCTC 719
                                Gaps
                                                                                                                                                                                                                                                                                                                                    CGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACA
                                                                                                                                                                                                                                                                      780 GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGCTGTTCCG
                                                                                                                                                                                                                                                      840 ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCT
                                                                                                                                                                                                         Length 7252;
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 Score 607.4; DB 20;
Pred. No. 6.8e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260 AAGCAGCAGATTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT90692 standard; DNA; 5865
 33.68;
97.58;
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                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid FBdelPRDSAF
Query Match
Best Local Similarity
Matches 617; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moloney murine
gene therapy;
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                                                                                                                                                                                                                                                                                                                  900
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Weiss RA;

Takeuchi Y,

Cosset F,

95GB-0017263

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Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation
                (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                        Claim 13; Fig 12; 79pp; English
                                           WPI; 1997-179287/16.
                                                                             re-initiation
                                Collins MKL,
     23-AUG-1995;
```

This sequence represents the recombinant expression plasmid FBdelPASAF.

This sequence is a packaging-deficient construct having a viral env gene

(In this case from RD114) and a selectable marker (SM). It is an example

(In this case from RD114) and a selectable marker (SM). It is an example

(In this case from RD14) and a selectable marker (SM). It is an example

(In this case from RD114) and a selectable marker (SM). It is an example

(In this case from RD114) and a selectable marker (SM). It is an example

(In this case from RD14) and a selectable strong comparison of the

(In the selectable stop codon is spaced from a start codon of the

(In and a GOI associated stop codon is spaced from a start codon of the

(In and a GOI associated stop codon is spaced from a start codon of the

(In this are that the SM protein is expressed as a result of

(In the viral env gene. By using helper constructs, such as the REV's,

(In the viral env gene. By using helper constructs, such as the REV's,

(In the viral gene, high titre retroviral vectors may be obtained. The

(In the susing full langth retroviral yeanness were

(In sold the doll langth retroviral genomes as helper genomes were

(In sold the doll langth retroviral genomes as helper genomes were

(In sold the doll langth retroviral genomes as helper genomes were

(In sold the doll langth retroviral genomes as the general section of

(In the cells in culture and the current packaging systems provide limited

(It reso of infectious retroviral packaging systems provide limited

(It reso of infectious retroviral packaging cell universement)

(In the section of directly select the best gay-pol-env-expressing

(In the section of the retroviral packaging cell lines overcome these problems. Sequence 5865 BP; 1492 A; 1602 C; 1390 G; 1373 T; 8 other;

.; 0 954 3752 tratcatytctggatccagatctgggcccatgcggccgcggatcgatnnnnacatgtgag 3811 894 834 655 TAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGCTGGCGTTTTTCCATA 714 GGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC 774 595 TTTACTGGCCTGCTCCCTTATCGGGAAGCGGGGCGCATCATATCAAATGACGCGCCGCTG 654 Gaps CGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTGGTGCGCTCTCCTG cgacaggactataaagataccaggegttteccectggaagetecetegtgegetetetg TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 895 ITTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG 33.4%; Score 604.4; DB 18; Length 5865; 91.4%; Pred. No. 4.6e-166; ; Indels Pred. No. 4.6e-166; 0; Mismatches 60; Conservative Similarity 638; Query Match Local 715 775 3932 835 Matches g οy q ŏ g ò g ò δ 셤 Ω g

4112

```
This sequence represents the recombinant expression plasmid FBdelPASAF.

This sequence is a packaging-deficient construct having a viral env gene

(in this case from the moloney murine leukaemia a virus) and a selectable

(marker (SM). It is an example of a recombinant expression vector (REV) of

the invention, used to create a packaging cell line. The REVs of the

invention comprise a gene of interest (GOI) and a SM gene. The SM gene is

invention comprise a gene of interest (GOI) and a SM gene. The SM gene is

creamsformed with two REVs of the SM gene to ensure that the SM protein is

from a start codon of the SM gene to ensure that the SM protein is

creamsformed with two REVs, both are replication deficient, one contains

the viral gag-pol gene, the other the viral env gene. By using helper

the viral gag-pol gene, the other the viral env gene. By using helper

constructs, such as the REV's, which are directly selectable and which

provide for high expression of the packaging cell lines are useful for gene

creators may be obtained. The packaging cell lines are useful for gene

therapy. Prior packaging cell lines using full length retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Packaging-deficient construct; viral gag-pol gene; packaging cell line; moloney murine leukaemia virus; MOMLV; viral env gene; helper construct;
                                                                                                                     1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation
                                                                                                                                                                                                   AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGGTGGTTTTTTT
TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
                GCIACACIAGAAGGACAGIATTIGGIATCIGCGCTCTGCTGAAGCCAGITACCITCGGAA
                                                            TTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG
                                                                                                                                                                                                                                                RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeuchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid FBdelPASAF coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 9; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                             AAT90689 standard; DNA; 6028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95GB-0017263
                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-179287/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        re-initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collins MKL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9708330-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                 AAT90689;
                                                                                                                                                                                                                                                                                                                                       13
              1015
                                           4172
                                                                         1075
                                                                                                      4232
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                                                                                                                                                                  4292
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                                                                                                                                                                                                                                                                                                                                       RESULT 1
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                                                                       best gag-pol-env-expressing cells. The new retroviral packaging cell
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                                                                                                                      8 other;
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                                                                                                                                                               Score 604.4; DB 18;
Pred. No. 4.7e-166;
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                                                                                     lines overcome these problems.
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nes 638; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systems provide limited titres of infectious retroviral vectors. Co-transfection with a plasmid encoding a SM does not directly select the
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                                    env gene; helper construct;
                ng-deficient construct; viral gag-pol gene; packaging cell line; murine leukaemia virus; MOMLV; viral env gene; helper construct
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Pred. No. 4.7e-166;
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Matches 638; Conservative
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                  Packaging-deficient
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represents the recombinant expression plasmid FBdelPASAF.
is a packaging-deficient construct having a viral env gene
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                                                                                                                                                                                        Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest; are selectable due to the in-efficiency associated with translation
                                                                               TTGAGTCCAACCCGGTAAGACACGACTTATCGCCCACTGGCAGCCACTGGTAACAGGA 1074
                                                                      GCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC 1014
                                             TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC
          TTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG
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Pred. No. 4.8e-166;
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Search completed: January 17, 2002, 12:05:08 Job time: 17895 sec

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Sequence 9, R Sequence 13, Sequence 13, Sequence 13, Sequence 3, R Sequence 3, R Sequence 3, R Sequence 13, S

Sequence 3, A Sequence 13, Sequence 8, A Sequence 8, A Sequence 8, A Sequence 1, A Sequence 8, A

Sequence:

Run on:

Searched:

Database

Result 8

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OTHER INFORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct
                                                                                                                                                                                                                      PCT - US93 - 08247 - 3
PCT - US94 - 14179 - 13
US - 08 - 212 - 463 - 8
US - 08 - 212 - 463 - 9
US - 09 - 075 - 019 - 8
US - 07 - 623 - 953 - 1
US - 08 - 675 - 566 - 8
                                                                                                                                                             US-07-941-372-3
US-08-165-301A-13
US-08-810-436-13
                                        PCT-US94-14030A-9
                                                                                               US-07-745-382-13
US-07-921-848-13
                                                         JS-07-989-847-13
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                                                                                                                                          US-08-115-680-3
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Sequence 8, Application US/09011745-

SERENTA INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Collins, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1996-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
SOFTWARE: PARENT ON NUMBER: GB9517263.1
EARLIER PILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 5865
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NAME/KEY: misc_feature
LOCATION: (3611)
OTHER INFORMATION: n is an
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3612)
OTHER INFORMATION: n is
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LOCATION: (3613)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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TYPE: DNA
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1 GGTACCTGCCACCATGGCGC......CTCGCACAGCCTCTCCCACA 1807
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-899-575-176
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PCT-US95-08743-176
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                                            Score 604.4; DB 4; Length 5865;
Pred. No. 8.8e-175;
0; Mismatches 60; Indels 0;
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; NAME/KEY: misc_feature
; LOCATION: (3801)
; CTHER INFORMATION: n is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; CATHOR INFORMATION: n is any nucleotide
US-09-011-745-8
                                                                                                                          Query Match 33.4%;
Best Local Similarity 91.4%;
Matches 638; Conservative
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Pred. No. 8.9e-175;
0; Mismatches 60;
TITLE OF INVENTION: Expression systems; FILE REFERENCE: 09/011,745; CURRENT APPLICATION NUMBER: US/09/011,745; CURRENT FILING DATE: 1998-06-22; EARLIER APPLICATION NUMBER: PCT/GB96/02061; EARLIER FILING DATE: 1996-08-23; EARLIER FILING DATE: 1995-08-23; NUMBER: OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (3774)
OTHER INFORMATION: n is any nucleotide
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ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: n is any
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                                                                                                                                                        PatentIn Ver. 2.0
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Matches 638; Conservative
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LOCATION: (3964)
OTHER INFORMATION: n is
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CEATURE: misc_feature
rocation: (3965)
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (3777)
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LOCATION: (3962)
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SEQ ID NO 5
LENGTH: 6028
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Sequence 5, Application US/09011745 Patent No. 6165715

US-09-011-745-5

RESULT

GENERAL INFORMATION:

APPLICANT: COLLINS, MATY KL APPLICANT: Weiss, Robin A APPLICANT: Takeuchi, Yasuhiro APPLICANT: Cosset, Francois-Loic

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                                                                                                            TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
                                                                                                                                                    TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG
                                                                                                                                                                                         GCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA
                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: Description of Artificial Sequence: Portion INFORMATION: construct
                                                                                                                                                                                                                                                                        APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francols-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        any nucleotide
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Sequence 6, Application US/09011745
Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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FEATURE:
NAME/KES: misc_feature
LOCATION: (3807)
OTHER INFORMATION: n is
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (3809)
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NAME/KEY: misc_feature
LOCATION: (3810)
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LOCATION: (3808)
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OTHER INFO
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Pred. No. 8.9e-175;
0; Mismatches 60;
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nucleotide
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NAMENKEY: misc_feature

LOCATION: (3997)

OTHER INFORMATION: n is any nu
FEATURE:

NAMENKEY: misc_feature

LOCATION: (3998)

OTHER INFORMATION: n is any nu
US-09-011-745-6
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91.48;
 any
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Best Local Similarity 91.4
Matches 638; Conservative
                                     NAMBLALL
LOCATION: (3995)
OTHER INFORMATION: n is an
FEATURE:
NAME/KEY: misc_feature
                                                                                                                         LOCATION: (3996)
OTHER INFORMATION: n is
INFORMATION: n is
         FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                             TTTCTCAATGUTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGCTTCGCTCCAAGCTGG 954
                                                                 775 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTG
                                                                                TTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC
                                                                                                                                                                                                                   Sequence 156, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: The Scripps Research Institute, Office of STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852 FILLION DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGCAAGCAGCATTACGCGCAGAAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/178,302 FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.4%; Score 604.4; DB 4; Length 6312; Best Local Similarity 91.4%; Pred. No. 9.1e-175; Matches 638; Conservative 0; Mismatches 60; Indels 0;
                                                                                             APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
NUMBER: OF SEQ ID NOS: 29
SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHER INFORMATION: n is any nucleotide US-09-011-745-7
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LOCATION: (4058)
OTHER INFORMATION: n is any nucleotide
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                                                   ; Sequence 7, Application US/09011745; Patent No. 6165715; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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NAME/KEX: misc_feature
NCATION: (4059)
OTHER INFORMATION: n is any
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NAME/KEY: misc_feature
LOCATION: (4060)
OTHER INFORMATION: n is
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LOCATION: (4249)
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LOCATION: (4061)
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LOCATION: (4248)
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LOCATION: (4247)
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                           RESULT 4
US-09-011-745-7
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Pred. No. 1.6e-174;
0; Mismatches 13;
                                                           ALTORNEL FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMUNICATION INFORMATION:
TELEPRONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
           APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 97.9%;
Matches 612; Conservative
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                                                 APPLICANT: LETTER, RICHARD A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5622138th Torrey Pines Road, Sulte 220, STREET: Mail Drop TPC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION WOMBER: US/VO/2/10,001
FILING DATE: 18-UL-1994
CLASSIFICATION 514
PRIOR APPLICATION DATE: 0508/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATE: 30-SEP-1993
PRIOR APPLICATION DATE: 30-SEP-1992
ATORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas A.163
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 34,163
TELEPHONE: 619-554-2937
TELECHORE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  Dennis R
Carlos F
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APPLICANT: Burton, APPLICANT: Barbas,
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TOPOLOGY: ci
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Sequence 170, Application US/08276852 Patent No. 5652138

RESULT 6
US-08-276-852-170/c
; Sequence 170, Appli
; Patent No. 5652138

circular

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MOLECULE TYPE: DNA (genomic) US-08-899-575-156
TOPOLOGY:
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                                                 1028 GGTAAGACACGACTTATCGCCACTGGCAGCACCACTGGTAACAGGATTAGCAGAGCGAG 1087
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 6979 ACCCCCGTTCAGCCCGACCGTGCCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5770440th Torrey Pines Road, Suite STREET: And Drop TPC8 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
ATOMORY/AGENT INFORMATION:
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TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
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MEDIUM TYPE: Floppy
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STRANDEDNESS:
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US-08-899-575-156
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  Length 13254;
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APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
APPLICANT: HUMAN INDURALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
TORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: Mail Drop TPC8
                                           Indels
                                           13;
Score 604.2; DB 1;
Pred. No. 1.6e-174;
0; Mismatches 13;
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      Ouery Match 33.4%;
Best Local Similarity 97.9%;
Matches 612; Conservative
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6799 GACAGTATTTGGTATCTGCGCTCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 6740
                                         668 TGAGAAAGAATTCCTGCAGCCGGCGTTGCTGGCGTTTTTCCATAGGCTCGGCCCCCC 727
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                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: The Scripps Research Institute, Office of Stabbressee: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Sulte 220, STREET: Mail Drop TPC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
                                                                                                                                                    GATTACGCGCAGAAAAAAAGGATCT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        Sequence 156, Application US/08899575 Patent No. 5804440
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
ITILE OF INVENTION: HUMAN NEUTI
TITLE OF INVENTION: TO HUMAN IN
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: double
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; MOLECULE TYPE:
US-08-899-575-156
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CITY: LA
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                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
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Pred. No. 1.6e-174;
0; Mismatches 13;
                                                                                                                                                                                                              PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UU-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 97.9%;
Matches 612; Conservative
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                       COMPUTER READABLE FORM:
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STRANDEDNESS: doubl
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RESULT 11
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                   6156 GCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTC 6215
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TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA 787
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                                                                        788 AAGAIACCAGGGGTITCCCCTGGAAGCTCCCTGTGCGCTCTCCTGTTCCGACCCTGCC
                                                                                                          AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCC
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Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA
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APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
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PatentIn Release #1.0,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                            Score 604.2; DB 1;
Pred. No. 1.6e-174;
0; Mismatches 13;
                                                                                                         REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
            FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
us 08/178,302
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                                                                                                                                                       TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic) US-08-899-575-170
                                                                                                                                                                                                                                                                                                                33.4%;
97.9%;
                                                                                                                                                                                                LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
          30-SEP-1993
                                                                                                                                                                                                                                                                                                               Query Match 33.4
Best Local Similarity 97.9
Matches 612; Conservative
APPLICATION NUMBER:
                                                                                                                                                                                                                                             circular
                                                                                                                                                                                                                TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                             TOPOLOGY:
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6799 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 6740
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                                                                                                                                                                                        TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBELICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.6e-174;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/276,852 FILING DATE: 18-JUL-1994 INFORMATION FOR SEQ ID NO: 170:
                                                                                                                               Sequence 170, Application PC/TUS9508743 GENERAL INFORMATION:
                                     6576 GATTACGCGCAGAAAAAAAGGATCT 6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.4%;
Best Local Similarity 97.9%;
Matches 612; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                               PCT-US95-08743-170/c
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; MOLECULE TYPE:
PCT-US95-08743-170
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                                                                                         HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
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                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.6e-174;
0; Mismatches 13;
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/08743 FILING DATE: 11-70L-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/276,852 FILING DATE: 18-70L-1994 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
APPLICATION:
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                                                                                                                       NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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Best Local Similarity 97.9%;
Matches 612; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                         TITLE OF INVENTION:
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                                     Sequence 156,
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APPLICANT: MALDONADO, Paul
APPLICANT: SALOWE, Marc
APPLICANT: SALOWE, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
                                                                                                                                                                                                                                                    1110 TICTIGAAGIGGIGGCCIAACTACGGCTACACIAGAAGGACAGIATITGGIAICTGCGCI 1169
                                                                                                                 TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
                                                                                                                                                                                   1050 CIGGCAGCAGCACTGGIAACAGGATIAGCAGAGCGAGGIAIGIAGGCGGTGCIACAGAG 1109
                                                                                                                                                                                                     546
                                                                                                                                                                                                                                                                                                                                                                                                           1170 CIGCIGAAGCCAGIIACCIITCGGAAAAAGAGIIGGIAGCICTIGAICCGGCAAACAAACC
                                                                                                                                                                                                                                                                                                                                          1230 ACCGCTGGTAGCGGTGGTTTTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA
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APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08906957 Patent No. 5856142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 683-0500
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APPLICANT: LEGOUX, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
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US-08-906-957-9
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APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: MALDONADO, Paul
APPLICANT: MALONADO, Paul
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
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                 Gaps
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                              - Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: FICHTER, RICHARD E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY AGENT INFORMATION:
                                                                         1268 GATTACGCGCAGAAAAAAGGATCT 1292
                                                                                           679 GATTACGCGCAGAAAAAAGGATCT 6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.**;
100.0%; Pr
                                                                                                                                                                                          Sequence 9, Application US/08594469
Patent No. 5700665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Me-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID No: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
                                                                                                                                                                                                                                                                                                                                                                       oacon & Thomas sirEET: 625 Slaters Lane CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 33.4 Best Local Similarity 100. Matches 603; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                 RESULT 13
US-08-594-469-9
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E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
E: P.C.
1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                          APPLICATION NO...

PILING DATE: 30.5EP-199/
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/533,717
FILING DATE: 26.5EP-1995
APPLICATION NUMBER: UP 6-268119
FILING DATE: 07-0CT-1994.
ATTORNEY.AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7335-001-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             7335-001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
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                                                                       USA
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TOPOLOGY: li
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                                                                     COUNTRY:
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                                                                                                                                                                                          Gaps
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                                                                                                                          Score 603; DB 2; Length 1905;
Pred. No. 1.3e-174;
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TITLE OF INVENTION: METHOD FOR PRODUCING ACTIVE HUMAN
TITLE OF INVENTION: ALANINE AMINOTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                33.4%; bcc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence I, Application US/08941647A Patent No. 595211 GENERAL INFORMATION:
APPLICANT: NAKAMURA, ATSUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TANAKA, TOSHIO
APPLICANT: MATUO, VISHI
APPLICANT: TANASE, SUMIO
APPLICANT: FUNATSU, MASAHIKO
APPLICANT: ETO, AKIRA
                                                                     DNA (genomic)
 SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                         Query Match 33.4
Best Local Similarity 100.
Matches 603; Conservative
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                                                                                0S-08-906-957-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGCAGCAGCACTGGTAACAGGATTAGCAGAGGTATGTAGGCGGTGCTACAGAG 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2763 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCCGACCGC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        870 TITICICCCTICGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCG 929
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,647A
FILING DATE: 30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.4%; Score 603; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.6e-174; Matches 603; Conservative 0; Mismatches 0;
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Search completed: January 17, 2002, 11:57:05 Job time: 17552 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-242-202A-28

US-09-242-202A-29

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US-09-422-202A-26

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US-09-18-478-5

US-09-19-535C-26

US-09-623-511-27

US-08-114-69-17

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US-09-628-730-56
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US-09-546-411A-48
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PCT-US99-06704-2
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US-08-447-430-42
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17
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1807
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/cgn2_6/ptcdata/2/pna/US097A_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US097A_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 42, Appli Sequence 42, Appli Sequence 42, Appli Sequence 56, Appl

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Sequence 28, Appl Sequence 29, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 7, Appl Sequence 5, Appl Sequence 5, Appl Sequence 7, Appl Sequence 17, Appl Sequence 27, Appl

Sequence 28,

Description

181   GTTGGGGGTGCAGCCGGCGCTTTACTGGCAACCAGCGGGGCGCCTTAAGG   240	361 TCCTGGCCCTGGAAGTTGCCACCTCCACCACCCTGTCCTAATAAATTAAGTT 420	481 CGGA           481 CGGA 541 AGAT	601 601 661	721 GCCCCCTGACGACCATCACAAAATCGACGCCCCCCCCCC	841 841 901	QY         961 TGCACGAACCCCCGTTCAGCCCGACCGCTGCCCCTATCCGGTAACTATCGTCTTGAGT 1020           Db         1	1081 1081 1141 1141 1201 1201
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3 18 US-09-485-737A-86 3 18 US-09-485-737B-86 0 3 US-07-671-058-7 2 29 US-09-742-373-10 ALIGNMENTS	n US/09242202 n, Edward L. n, Peter J. NN NOVEL VECTOR FOR POLYNUCLEOTIDE VACCINES 129.	ADDRESSE: MOGGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTY: USA ZIP: 10154 TER READABLE FORM:	PATIBLE -DOS/MS-DOS US/09/242,202	APPLICATION NUMBER: US60/023931 FILING DATE: 14-AUG-1996 ATTORNEY/AGENT INFORMATION: NAME: KATHRYN M. BROWN REALSCYARATION NUMBER: 34556 REFERENCE/DOCKET NUMBER: 2026-4236US1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPONY: (212) 758-4800 MENERS ARE	TELERY: 1217) 71 01 01 01 01 01 01 01 01 01 01 01 01 01	NO 21 22 31 31 31 31 31 31 31 31 31 31 31 31 31	vative ), argecegearl argecegearl argecegearl argecegearl iiiiiiiiiiiii grercaagcarc arcaagcarc aacaagcarc
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88888888888888888888888888888888888888	Application US, ORMATION: ANT: Nelson, E Melson, E INVENTION: OF INVENTION: OF SEQUENCES:	DORESSEE: DDRESSEE: TYEET: 345 TY: NEW Y TATE: NEW OUNTRY: US IP: 10154 ER READABI	EDIUM TR OMPUTER: PERATING OFTWARE: T APPLICA PPLICATING DA' APPLICAT	PPLICATI ILLING DA IBY/AGENT IAME: KAT IEGISTRAT EFERENCE EFERENCE ELEPHONE ELEPHONE	ELEX. 4.2 1 FOR SEQ 1 FOR SEQ 1 CE CHARA 1 SENGTH: 1 1 YPE: nuc 1 TRANDEDN 1 OPOLOGY: 1 LE TYPE:	IETICAL: SENSE: NC S8	Conserved
6.6.6. 4.4.4.	PP1 RMA NT: NT: OF	CONTROL MORGAN STREET: 345 PARK A CITY: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10154 COMPUTER READABLE FORM:	COMPUTER: IDAN PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: MS WORD 97 CURRENT APPLICATION DATA:  PRIOR APPLICATION NUMBER: PILING DATE: 01-NOV-PRIOR APPLICATION DATA:	APPLICATI FILING DA FILING DA ATTORNEY/AGENT NAME: KAT REGIESTRAT TELECOMMUNICAT TELECOMMUNICAT TELEBRONE	INFORMATION FOR SEQ ID NO: 28 SEQUENCE CHARACTERISTICS LENGTH: 1807 base p TYPE: nucleic acid STRANDEDNESS: singl TOPOLOGY: unknown MOLECULE TYPE: cDNA	HYPOTHETICAL: NO ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ -09-242-202-28 QUETY MATCH 100.0%;	Matches 1807; Conservations 1807; Conservations 1807; Conservations 1 GGTACCTGCCACC.  1 GGTACCTGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1807 base pairs
 TELEFAX: (212) 751-6849
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100.0%;
                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
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Matches 1807; Conservative
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KATHRYN M. BROWN
REGISTRATION UNDBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/242,202A
FILING DATE: 20-Apr-2000
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR
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FILING DATE: 14-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09242202A GENERAL INFORMATION:
APPLICANT: Nelson, Edward L.
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CORRESPONDENCE ADDRESS:
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                                                     CCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGGCGCTTTCTC 900
                                             AATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG 960
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                                                                                         POLYNUCLEOTIDE VACCINES
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NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1878-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.6%; Score 1583.2; 99.8%; Pred. No. 0;
                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: MORGAN & FINNEGAN, L.L.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202
FILING DATE: 01-Nov-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-242-202-29
                                                      Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR
                                                                                                                                                                                                                                                                               MEDIUM TYPE: DISKETTE, 3.5 I COMPUTER: IBM PC COMPATIBLE
Sequence 29, Application US/09242202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 2308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 751-6849
TELEX: 421792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
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Best Local Similarity 99.8
Matches 1585; Conservative
                                                                                                             SEQUENCES:
                                         APPLICANT: Nelson,
                                                                                                                                                                                                                            COUNTRY: USA
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                                                                                                                                                                                                                                          ZIP: 10154
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ANTI-SENSE:
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                                            TTCGCTCCAAGCTGGGCTGTGCACGAACCCCCGGTTCAGCCCCGACCGCTGCGCCTTAT
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                                    AATGACGCCCCCTGTAAAGTGTTACGTTGAGAAAGAATTCCTGCAGCCCGCCGCGTTGC
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1660 TATGATACCGGCCAATGCTTGGTTGCTATTTTGGAAACTCCCCTTAGGGGATGCCCCTCA
                       2161 TATGATACCGGCCAATGCTTGGTTGCTATTTTGGAAACTCCCCTTAGGGGATGCCCCTCA
                                                                                      ACTGGCCCTATAAAGGGCCAGCCTGAGCTGCAGAGGATTCCTGCAGAGGATCAAAGACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (712) 758-4800
TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202A
FILING DATE: 20-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FINNEGAN, L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.6%; Score 1583.2;
99.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL VECTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
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                                                                                                                                                                            1780 ACGIGGACCICGCACAGCCICICCCACA 1807
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                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09242202A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2308 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                         Peter J.
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nelson, Edward
Nelson, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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Matches 1585; Conservative
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202
FILLING DATE: 01-Nov-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               FINNEGAN, L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL VECTOR FOR POLYNUCLEOTIDE VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    ACGTGGACCTCGCACAGCCTCTCCCACA 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHERICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                        1780 ACGTGGACCTCGCACAGCCTCTCCCACA 1807
                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/09242202 GENERAL INFORMATION:
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ADDRESSEE: MORGAN & FINN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                         Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: NEW YORK
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ZIP: 10154
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US-09-242-202-27
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REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFRAX: (212) 751-6849
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REFERENCE/DOCKET NUMBER: 2026-4236US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/242,202A FILING DATE: 20-Apr-2000 PRIOR APPLICATION DATA:
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                     Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
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TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09242202A GENERAL INFORMATION:
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LENGTH: 1547 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: KATHRYN M. BROWN
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SEQUENCE DESCRIPTION: SEQ
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99.9%;
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                                      Score 1310.4;
Pred. No. 0;
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                                      72.5%;
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Best Local Similarity 99.9
Matches 1311; Conservative
US-09-242-202-27
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Length 7252;
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kingsman, et al
TITLE OF INVENTION: Retroviral Vectors
FILE REFERENCE: 6/4523-2006
CURRENT APPLICATION NUMBER: US/09/238,356
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: PCT/GB/03876
PRIOR FILING DATE: 1998-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATABASE ACCESSION NUMBER: AX003206
DATABASE ENTRY DATE: 2000-08-24
RELEVANT RESIDUES: (1)..(7252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence, plass
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) . (7522)
OTHER INFORMATION: Plasmid vector
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ; Sequence 27, Application US/09238356; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
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Best Local Similarity 97.5
Matches 617; Conservative
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US-08-480-120-15
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1020 TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACAGGATTAGC 1079
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                                                                                                                                                          APPLICANT: Joliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Pulito, Virginia L.
AITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,120
FILING DATE: UN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: DiGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
TELECOMUNICATION INFORMATION:
TELEPAN: (516) 742-4343
TELEPAN: (516) 742-436
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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US-08-480-120-15
Sequence 15, Application US/08480120
GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
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                                                                                             Length 7073;
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GENERAL INFORMATION:
APPLICANT: Joinffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Linda K.
APPLICANT: Linda K.
APPLICANT: Linda K.
APPLICANT: APPLICANT: Virginia L.
TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 20
                                                                                                                                              Indels
                                                                                                                                                13;
                                                                                                DB 8;
                                                                                             Score 604.2; DB 8;
Pred. No. 1.8e-167;
0; Mismatches 13;
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                                                                                             Query Match 33.4%;
Best Local Similarity 97.9%;
Matches 612; Conservative
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MEDIUM TYPE: Floppy disk
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930 GIGIAGGICGIICGCICCAAGCIGGGCIGIGTGCACGAACCCCCCGTICAGCCCGACCGC 989
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llarity 100.0%; Pred. No. 1.3e-167;
Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/09/242,202

FILING DATE: 01-NOV-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US60/023931

APPLICATION NUMBER: US60/023931

FILING DATE: 14-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: KATHRYN M. BROWN

REFERENCE/DOCKET NUMBER: 34556

REFERENCE/DOCKET NUMBER: 3450

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 COMPOTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
                                                                                                                                                                                     POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-242-202-26
                                                                                                                                                      Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR
1855 GATTACGCGCAGAAAAAAGGATCT 1879
                                                                                                Sequence 26, Application US/09242202
GENERAL INFORMATION:
APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-48(
TELEFAX: (212) 751-6849
TELEX: 421792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                          STATE: NEW YORK
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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Matches 603; Conserv
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                                                                        RESULT 10
US-09-242-202-26
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                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 1.8e-167;
0; Mismatches 13;
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                                                               CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/480,12C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                ATTORREY AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION UNBER: 31,346
REFERENCE/DOCKET UNBER: 9598
TELECOMMUNICATION INFORMATION:
TELEFAM: (516) 742-4343
TELEFAM: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.4%;
97.9%;
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7864 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.4 Best Local Similarity 97.9 Matches 612; Conservative
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
US-08-480-120-20
                                                    SOFTWARE:
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                                                                                                                                            6 GCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGACGACAAAAATCGA
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                                                     Length
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APPLICANT: Ruffner, Michael L.
APPLICANT: Pierce, Michael L.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zahdong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: 76678.PCT
CURRENT APPLICATION NUMBER: PCT/US99/06742
CURRENT APPLICATION NUMBER: 60/079,792
EARLIER FILING DATE: 1998-03-28
SOFTWARE: Word97
SEQ ID NO 7
                                                   33.4%; Score 603; DB 16; I 100.0%; Pred. No. 1.3e-167; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application PC/TUS9906742 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                       Matches 603; Conservative
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OTHER INFORMATION: pASlib
                                                                       Similarity
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   US-09-242-202A-26
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Best Local
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                                                                                                                        1050 CTGGCAGCACCACTGGTAACAGGATTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAG 1109
                                                                                                                                                                                                                                                                 246 GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC 305
                                                                     990 TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCCAACCCGGTAAGACACGACTTATCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/242,202A
FILING DATE: 20-Apr-2000
PRION APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US60/023931
FILING DATE: 14-AUG-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34556
REFERENCE/DOCKET NUMBER: 2026-4236US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson, Peter J.
TITLE OF INVENTION: NOVEL VECTOR FOR POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09242202A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nelson, Edward L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 26:
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ZIP: 10154
COMPUTER READABLE FORM:
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GRANISM: Escherichia coli
US-60-118-478-5
Conservative
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US-60-118-478-5
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  Matches
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                                                                            GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC 989
                                                                   GCCGCGTTGCTGGCCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA 749
                                                   Gaps
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                                Length 2077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McNeish, John D. APPLICANT: McNeish, Michael K TITLE OF INVENTION: Transgenic Animals Expressing Human | FILLE REFERENCE: PC10142a CURRENT APPLICATION NUMBER: US/09/496,445 CURRENT FILING DATE: 2000-02-02 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 5 LENGTH: 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 603; DB 18; Pred. No. 2.5e-167;
                                33.4%; Score 603; DB 1; La
100.0%; Pred. No. 2.3e-167;
                                                    0; Mismatches
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100.0%;
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                                            Best Local Similarity 100.
Matches 603; Conservative
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US-09-496-445-5
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Best Local Similarity
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tct 2039
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US-09-496-445-5
        PCT-US99-06742-7
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GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA 749
              930 GIGTAGGICGTICGCICCAAGCIGGGCIGIGIGCACGAACCCCCCGIICAGCCCGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 603; DB 44;
Pred. No. 2.5e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
33.4%; Score 603; DE
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 603; Conservative 0; Mismatches
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TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCA 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1110 TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230 ACCGCTGGTAGCGGTGGTTTTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA 1289
              659 tgcgccttatccggtaactatcgtcttgagtccaacccggtaagacacgacttatcgcca 718
                                                                                                                                                                                                                                                                                                                                                                                              719 ctggcagcagcactggtaacaggattagcagagggaggtatgtaggcggtgctacagag 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 TITCICCCTICGGGAAGCGTGGCGCTITCICAAIGCICACGCTGIAGGIATCICGGTICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTCAAGTCAGAGGGGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT
                                                                                                                                                                           539 tttctcccttcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagttcg
                                                                                                                                                                                                                GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGGTTCAGCCCGACCGC
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/919,535C
FILING DATE: 19920723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-07-919-535C-26
SQUENCE 26, Application US/07919535C
GREERAL INFORMATION:
APPLICANT: Haas, Werner
APPLICANT: Honziker, Willi
TITLE OF INVENTION: SOLUBLE KIT LIGANDS
UMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: RAN 4105/142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91810609.7 FILING DATE: 30-JUL-1991 ATTORNEY/AGENT INFORMATION: NAME: Kass, Alan P. REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
COUNTRY: United States
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoffmann-La Roche
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 199207:
CLASSIFICATION: 435
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tct 961
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976 GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCCGACCGC 1035
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                                                                                                                                                                                                                                                                                        /note= "Recognition site for restriction enzyme Nco!"
                                                                                                                                                                                                                                                                                                                                                                                        /note= "Recognition site for
restriction enzyme HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.4%; Score 603; DB 3; Le
100.0%; Pred. No. 2.5e-167;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of E. coli
expression plasmid
poc 56/RBS II, Ncol"
                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 2577 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..2577
OTHER INFORMATION: fnote
OTHER INFORMATION: expre
OTHER INFORMATION: expre
                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 121..126
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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                                                                                                                                                                                                       ORGANISM: Escherichia
                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 141.146
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                        linear
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                                                                                                                                            TOPOLOGY:
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Search completed: January 17, 2002, 15:14:36 Job time: 22788 sec

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